## STIC-Biotech/ChemLib

From:

Sent:

Ibrahim, Medina A. Tuesday, November 05, 2002 1:27 PM STIC-Biotech/ChemLib 09/771, 045

To: Subject:

## Please search the following:

1. SEQ ID NO:35

2. oligo search of at least 20 contiguous bases of SEQ ID NO:35. Please search both commercial and issued patents databases. Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9A12 mailbox-9E12 (703)306-5822

> POINT OF CONTACT: PAUL SCHULWITZ **TECHNICAL INFO. SPECIALIST** CM1 6B06 TEL. (703) 305-1954

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:/	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 1//7	Bibliographic:	DRLink:
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

and includes of use

patent: US 6211434-A 35 03-APR-2001; AF429315 Homo sapi AF429315 Homo sapi AB038563 Canis fam AL684658 Penicilli PAT 08-AUG-2001 AL161755 Streptomy AP003002 Mesorhizo S62734 monoamine o X15609 Bovine mRNA AF230492 Streptomy Streptomy Sinorhizo Sequence Seguence Sequence Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AR145464 AR145468 AR145469 AR145461 AR145461 AR145489 AR145481 linear DNA 1929 bp Sequence 35 from patent US 6211434. AR145464. AR145464.1 GI:15107331 ALIGNMENTS SUMMARIES AR145464
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 39 03-APR-2001;
Location/Qualifiers
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Pred. No. 0;
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AR145466
AR145466.1 GI:15107333
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97.8%;
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Best Local Similarity 97.8
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       GGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGCTAGCCTGGTGCC
AGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGG
                            AGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAAC
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Duvick, J.P., Gilliam, J.T. and Maddox, J.R.
Amino polyol amine oxidase polynucleotides
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Pred. No. 0;
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Location/Qualifiers
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AR145468.1 GI:15107335
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Best Local Similarity 95.9
Matches 1850; Conservative
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AR145468
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 41 03-APR-2001;
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Duvick J.P., Gilliam.J.T. and Maddox,J.R.
Manno polypol amine oxidase polynucleotides and methods of use
Patent: US 6211434-A 22 03-APR-2001;
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ARI44457.1 GI:15107324
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                                         Score 1602.6;
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ACCESSION AR145484 VERSION AR145484.1 GI:15107351 KEYWORS SOURCE OUKNOWN ORGANISM UNKNOWN  REFERENCE 1 (bases 1 to 1803) AUTHORS JOUGNAL Patch of 10 lamine oxidase polynucleotides and related polypeptides JOURNAL Patent: US 6211435-A 22 03-APR-2001; FEATURES 1.1803 SOURCE 1.1803 ACCESSIONT 424 a 501 c 502 g 376 t	Ouery Match  83.1%; Score 1602.6; DB 6; Length 1803;  Best Local Similarity 91.7%; Pred. No. 0;  Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;  Oy 1ATGGACTTGCAGCGAGCTACATCACCACCAACGTCGCCTCCCAGCAGGTATTCC 60	121 GACGCTTTGGGCGTGACAGACCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180	DESCRIPTION	QY         541 CTGAGGGTACAATCGGGCAGGACGACTATCAACGACCTCGGGGTGGGT	OY 721 CCTTATGGTGACTCCCGGTAAGCACAATCCCACTTGTGATGAGACCTCTGTCGAGTGT 780 
961 AAACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACAGCGCTCTGCTCGGTGTGGA 1020	1201   TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGGCACCTCAACACCCCGGTCGCT   1260	1381 CUTTTCCGGGGAGAAGGGATGGGGGAAAATTCTATCCTGGGTATAGGAG 1440  1255 CCTTTCCGGCGAGAAGCATGGCGGAAAATTCTATCCTGGGCTACTATAGCAG 1314  1441 ATAGTCTTCGTATGGGCAACCGTGGTGGCGGAACAATTCTTCGGGCGTCCTCCAA 1500  1441 ATAGTCTTCGTATGGGACAACCGTGGTGGCGGAACAAGGCTTCTCGGGCGTCCTCCAA 1500  111111111111111111111111111111111	AG 1494 AA 1680 AA 156 AA 1554		RESULT 8 AR145484 LOCUS AR145484 DISCUS AR145484 DEFINITION Sequence 22 from patent US 6211435.

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Db 1735 GAA(	RESULT 9 AR145462 LOCUS DECINITION SG ACCESSION AN VERSION VERSION COURCE COURC	AUTHORS DI AUTHORS DI TITLE AN JOURNAL PR FEATURES SOURCE BASE COUNT	Query Match Best Local S Matches 176	DD 688 ATG Qy 61 CAC; DD 748 CAC QY 121 GACG	241 241 928	301 988 361 1048	421 1108 481 1168 541 1228
781 AGAATACAGTCACTGACTCCAGCTGAGCGGGGGGTTGCAAGTGCACTTGC 840	901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGGACTACTGTGAGAAGGACCT 960	1081 TAATATTGTCGGACAAGAAGACGGCGGCAGTATATGCGATGCAAACAGGTGCGTG   1081 TAATATTTCTCGACAAGAAGACGGCGGCAGCATATGCGATGCAAAACAGGTGCGTG   1082 TAATATTTCTCGGACAAGAAGACGGCGGGCAGTATATGCGATGCAAAAAAAA	1201 TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCCCCACCCCGTCGCT 1260	1321	1441 1315 1501 1375	1561 TCCATTACCTGTTCATGGTCGGACCCGGACGGAAGTGGTCCCAACAGTCCAAGCAG 162	1681 GTCCCAAGGCCGCAACGGCCTCCAAATCGAGGCACCAGTATTTCCAAGGA 1740 11555 GTCCCAAGGCCGCAACGGCCTCCAAATCGAGGCACCAGTATTTCCAAGGA 1740 1151111111111111111111111111111111111
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Unknown.
Unclassified.
1 (bases 1 to 2490)
Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides and related polypeptides
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Patent: US 6211434-A 32 03-APR-2001;
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Sequence 32 from patent US 6211434.
AR145462. GI:15107329
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Db 2242 GFCC Qy 1741 GCFC Db 2302 GCFC Qy 1801 CCGI	2362	2422	07 1921 GCAC           Db 2482 GCAC		ACCESSION AN VERSION AN KEYWORDS	ORGANISM UT  REFERENCE 1		FEATURES SOUICE BASE COUNT	ORIGIN Query Match Best Local &	accines 1		121	808 181	241	301	DD 988 TTT QY 361 GAA DD 1048 GAA
	TCGAGTGT 780	GCACTTGC 840           GCACTTGC 1454	CCCAAGC 900                 CTCAAGC 1514	AAGGACCT 960           AAGGAACT 1574	GGTGTGGA 1020            GGTGTGGA 1634	GGTCTCAG 1080           GGTCTCAG 1694	NGGTGCGTG 1140	AGTCGATT 1200	CCGTCGCT 1260	TGTTCCGA 1320	TTTCACCA 1380            TTCACCA 1941	ATAGCAAG 1440 	STCCTCCAA 1500 	GGCGAATGG 1560    1      GGCAATGG 2121	FCCAAGCAG 1620            CCAAGCAG 2181	3GGCCCAA 1680           3GGCCCAA 2241  TCCAAGGA 1740
AATGACAGCAACGAAAGGGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGGGAGGCGAGGTTTTGAAGGGGGGAGGGGGAGGGGAGAGAGA	CCTTATGGTGACTCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 	AGAATACAGTCACTGCCACTTCGTCCAGCTGAGCGAGGAGGAGGTTGCAAGTGCACTTGC	GGAACTCCTCCCCGTATGGTCTCAGCTGATCGAGGTATAGCCTTGAAGACCCCCAAGGC	GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT	AAACTIGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACACGCGCTCTGCTCGGTGTGGAACTIGGTTGTTGTTGTTCGGTGTTGGAAACTTGCCTGCTCGGTGGTAGGAAACCAGATCACACGCGGTCTGGTTGGT	AGCCCACGAGATCAGCATGTTTTCTCACGACTACATCAAGAGTGCCACGGTGTCAG	TAATATIGICTCGGACAAGAAGACGGCGGGCAGTATATGCGATGCAAAACAGGTGCGTG 	CGGTGTCCTCTCAGGTAGGGGACTCGTTCTTAGTGGTCATTCCAGGTATGCAGTCGATT	TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCGGTCGCT	GGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCGCCGTGTTCCGA	AGCAAAAAGGGGGGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCA	CCTCTTCCGCCGGAAGAAGATTGGCGGAAAAATCTATCCTGGGTACTATAGCAAG 	ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA	TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG 	TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGCGGTCCAAGCAG	GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
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Unclassified.

1 (bases 1 to 2490)

1 (bases 1 to 2490)

Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use

Patent: US 6211435-A 32 03-APR-2001;

Location/Qualifiers
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qa	da da	ζΟ QO	QQ	da da	QQ Dp	Qy	da	RES ARI	DEFI ACCE VERS	SOUR OR REFE	Au TI TO	FEAT	ORIG Qu Be		DP QY	Db Qy	DP	QQ P
GTTGCGGACGTGGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGACGCCACGCAAAGTC 480 GTTGCGGACGTGGAAGTGGTAGGCACACACACACACACAC	F 540	1	AATGACAGCAACCAAAGGGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGGGAG 660 	ACAGCT 720         ACAGCT 140	78	CACTIGC 84          CACTIGC 14	GAACTCCTCCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900 	CAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960 	AAACTIGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACACGCGCTCTGCTGGGTGTGGA 1020 	AGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGGTCTCAG 1080 	TAATATTGTCTCGGACAAGAAAGACGGCGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140 	CGTTTCTTAGTGGTCATTCCAGGTATGCAGTCGATT	TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCCGTCGCT 1260 	GGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCGCGTGTTCCGA 1320 	AGCAAAAAGGTGGTGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCA 1380 	CCTCTTCCCGCCGAGAAGCAAGCATGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG 1440 	CTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGCTTCTCGGGGGTCCTCCAA 1500 	CTCATTTGCCAGAGATACCAGCATCGAAGTCGGTTGGC 1560
421 GTTGCGGACGTGGTAGTGGTGGGC 	81 68	541 CTGAGCGTACAATCGGGTCCCGGC 	601 AATGACAGCAACCAAAGGGAAGTA 	661 CTCCAGAGGACGACCGGAAATTCA 	721 CCTTATGGTGACTCCCGGTAAGC.                  1   1  1  1  1  1  1	781 AGAATACAGTCACTGACTCCACTT	841 GGAACTCCTCCCGTATGGTCTCA 	901 GAGCCTCAGGGGAAGCGGCTCGA 	961 AAACTTGCCTGCTGTTCTCAGCGT 	1021 AGCCCACGAGATCAGCATGCTTTT.	1081 TAATATTGTCTCGGACAAGAAAGA( 	1141 CGGTGTCCTCTCAGGTAGGGAACTC	1201 TGCCATGCCATGTCAAAGGAACTTC 	1261 GGAATTGAGCAGTCGGCGTCCGGCT 	1321 AGCAAAAGGTGGTGGTTCGTTAC 	1381 CCTCTTCCGGCGAGAAGCAAGCAI 	1441 ATAGTCTTCGTATGGGACAACCCGT 	1501 TCGAGCTGTGACCCCATCTCATTTG
oy G	Qy	Qy Db	Qy Dp	Qy Dp	0y Dp	Oy Dp	90 da	Qy Gp	Qy Dp	Oy Dp	Oy Dp	Oy Dp	Qy	Oy Dp	Oy Dp	Qy Dp	O.y Db	ò

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Unclassified.

1 (bases 1 to 1442)

1 (bases 1 to 1442)

1 (bases 2 to 1442)

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2 (bases 4 to 111 to 1442)

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                                                        GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGGCCCAA
                                                                                                           GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCCTCAGAACG
                                                                                                                                                                                                                  2302 GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG
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                                                                                                                                                                                                                                                                        415 GACAACGTIGCGGACGTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGACGGCACGC
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Sequence 7 from patent US 6211434.
AR145448 1GI:15107315
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1248	OY 1/95 A   DD 1308 A	1368	Qy 1915 G	Db 1428 G	RESULT 12 AR145475 LOCUS	ACCESSION VERSION KEYWORDS	ORGANISM ORGANISM REFERENCE	TITLE JOURNAL	FEATURES SOURCE BASE COUNT	Query Mat Best Loce	Qy 415 C	Db 1 (	Oy . 475 P		Db 121 2	Db 181		Db 241	UY /13	Qy 775	Db 321	ń -	7
655 GGCGAGCTCCAGAGGACGACGGAAATTCAATCCATCAAGCACAAGACGGTACAACCACT 714 	715 ACAGCTCCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTC 774		c	835 ACTIGCGGAACTCCTCCCCGTATGGTCTCAGCTGATGGAGGTATAGCCTTGAAGACCC 894	895 CAAGGCGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAA 954	955 GGACCTAAACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACACGCGCTCTGCTCGG 1014 	1015 TGTGGAAGCCCACGAGATCAGCATGTTTTTCTCACCGACTACATCAAGAGTGCCACCGG 1074	1075 TCTCAGTAATATTGTCTCGGACAAGAAAGACGGCGGCAGTATATGCGATGCAAACAGG 1134 	1135 TGCGTGCGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGTATGCAG 1194 .	1195 TCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCC 1254 [	П	08 GICGCIGARATIGAGCAGICGGCAICCGGCIGIACAGIACGGGCCICGGGCCICGGGCGCGGGGGGGG	11111111111111111111111111111111111111	1375 TCACCACCTCTTCCCGCCGAGAAGCATGGCGGAAAATCTATCCTCGGCTACTAT 1434	1435 AGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTC	948 AGCAAGATAGTCTTCGTATGGGACAAGCCGTGGTGGCGCGAACAAGGCTTCTCGGGGGGTC 100	1495 CICCAATCGAGGTGTGACCCCATCTCATTTGCAACAGATAACCAGAGTGGAACG 1554	1555		161	1128 ANGCANGIACGACAGAGCCGGCCAACGTGCTGGAGTGGTGGAGGAGCAGCAGTATTTC 173		7 1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
Qy Db	Qy	Qy	Op	Oy Db	Qy Db	Qy Db	Qy Db	Qy Db	QY Db	Qy Db	QY		g g	QY	Qy	qq	QY Db	QY	Q	QY	oy oy	qq	QY

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1 (bases 1 to 1442)
Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Amino polypol amine oxidase polynucleotides and related polypeptides and methods of use Patent: US 6211435-A 7 03-APR-2001;
Location/Qualifiers
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                                     AAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCG 594
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TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
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AR145459		SOURCE UNKNOWN. ORGANISM UNKNOWN. UNCLASSIFIED. REFERENCE 1 (bases 1 to 2	AUTHORS DUVICK, J.P., G11 TITLE AMINO POLYOL ami and methods of u JOURNAL Patent: US 62114	9	ORIGIN Query Match Best Local Similarity 90	QY 409 ACCCAGACAACGTTGCG	469	1642	589	649	1822	1882		1929 889	949	DD 2049 TGAGAAGGAACTAAACTT QY 1009 GCTGGGTGGAAGCCCA Db 2109 GCTCGGTGGTGAAACCCA	1069
QY 895 CAAGGCGACCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAA 954	Qy     955 GGACCTABACTTGCCTGCTGTTCTCAGCGTGGCAAACCAGATCACAGGCGCTCTGCTCGG 1014       11	QY 1015 TGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACGACTACATCAAGAGTGCCACCGG 1074	QY 1075 TCTCAGTAATATTGTCTCGGACAAGAAAGACGGCGGCAGTATATGCGATGCAAACAGG 1134 	OY 1135 TGCGTGCGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGTATGCAG 1194	<pre>Qy 1195 TCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCC 1254</pre>	<ul> <li>Qy 1255 GTCGCTGGAATTGAGCAGTCGGCTGCTGTGTATAGTACGATCGGCCTCGGGCCCCGTG 1314</li> <li>IIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIII</li></ul>	Qy 1315 TICCGAAGCAAAAAGGIGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATT 1374	OY 1375 TCACCACCTCTTCCGCGAGAAGCAAGCATGGCGGAAAAATCTATCCTCGGCTACTAT 1434 	Qy         1435         AGCAAGATAGTCTTCGTATGGGACAACCGTGGTGGCGGACAACAAGGCTTCTCGGGCGTC         1494           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	dy     1495     CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGATACCAGCATCGAAGTCGATCGG     1554       Db     1008     CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGACGTCGATCGA	OY 1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGACGGA	Qy       1615       AAGCAGGTACGACAAAAGTCTGTGTGGGACCAACCGCGCGCG	Qy 1675 GCCCAAGTCCCAGAGCCGGCCAACGTGGTCGAAATCGAGTGGTCGTCGAGCAGCAGTATTC 1734	QY 1735 CAAGGACTECGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGGGTC 1794	OY 1795 AGAACGCCGTTCAAGTGTGTTCATTCGTTGGAACGCACGTCTTTAGTTTGGAAGGG 1854	OY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914  111111111111111111111111111111111	Qy 1915 GTGCCAGCAGCATAG 1929 
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	SOURCE 129/b /organism="unki	OKIGIN Query Match Best Local Similarity 90.2%; Pr	1372; Conserva ACCCCAGACAACGTT	Db 1582 AGCAAAGACAAGGTTGGGGGGGGGGGGGGGGGGGGGGGG	1642	1702	1762	709	1882		1929 889	1989	2049	Db 2109 GCTCGGTGTGGAAGCCCACGAGATCA Qy 1069 CACCGGTCTCAGTAATATTGTCTCGG Db 2169 CACCGGTCTCAGTAATATTTCTCGG	QY 1129 AACAGGTGCGTGCGGTGTCCTCTCAG	1189	Db 2236 ATGCAGTCGATTGCCATGCCATG Qy 1249 ACCCCGTCGCTGGAATTGAGCAG	Db 2296 ACCCCGTCGCTGAAATTGAGCAGTC	Qy 1309 GCCGTGTTCCGAAGCAAAAAGGTGGT	
R SOURCE OF STATES.	1129 AACAGGIGCGIGCGIGICCTCTCAGGIAGGGGACTCGTTTCTTAGTGGICATTCCAGGT 118 	1189 ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC 124	1249 ACCCCGGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCTCGGGCTCGGCTCGGCTCGGCTCGGCTCGGCGCCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCCTCGGCGCCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCGCTCGGCCTCGGCCTCGGCCTCGGCCTCGCGCCTCGGCCTCGGCCTCGGCGCTCGGCCTCGCGCCTCGGCCTCGCGCCTCGGCCTCGCGCCTCGCGCCTCGCGCCTCGCGCCTCGCGCCTCGCCGC	1309 GCCGTGTTCCGAAGCAAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTG 	1369 ACATTITCACCACTCTTCCCGCCGAGAAGCAAGCATGGCGGAAAAATCTATCCTCGGC	1429 TACTATAGCAAGATAGTCTTCGTATGGGACAACCGGTGGTGGCGCGGAACAAGGCTTCTCG	1489 GGCGTCCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTC 1	1549 GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGCACCCGGACGGA	1609 CAGTCCAAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGGCAGCGTACGAGAAC	1669 GCCGGGGCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTGGTCGAAGCAGCAG 172	1729 TATTTCCAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCG 178	1789 GCGCTCAGAACGCCGTTCAAGTGTTCTTTTCGTTGGAACGGAGGCGTCTTTAGTTTGG 184	1849 AAAGGGTATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCT 	1909 AGCCTGGTGCCAGCATAG 192 		AR143400 25 from patent US 6211435.  1 AR145486.1 GI:15107353		Unclassified. 1 (bases 1 to 2976) Duvick J.P., Gilliam, J.T.,	Amino polyol amine oxidase and methods of use Patent: US 6211435-A 26 03-	FEATURES Location/Qualifiers

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                                                             23;
                                     core 1212.2; DB 6;
red. No. 1.4e-313;
Mismatches 23;
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        GCCGGGGCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAG
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                                                          GGCGTCCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTC
                                                                                      GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAA
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Pred. No. 1.4e-313;
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Search completed: November 12, 2002, 04:43:39 Job time : 5111 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Exophiala spinifer	Exophiala spinifer	Exophiala spinifer	Rhinocladiella atr	Rhinocladiella atr	Rhinocladiella atr	Exophiala spinifer	DNA encoding a ful	DNA encoding GST-t
SUMMARIES	QI	AAZ58382	AAZ58383	AAZ58384	AAZ58386	AAZ58387	AAZ58385	AAZ58402	AAZ60641	AAZ58407
		21	21	21	21	21	21	21	21	21
	Query Match Length DB	1929	1929	1930	1928	1928	1928	1803	1803	2490
æ	Query Match	100.0	8.66	96.0	92.9	92.7	92.7	83.1	83.1	82.7
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## ALIGNMENTS

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Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                               Exophiala spinifera amino polyol amine oxidase ESP002_C2 DNA.
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/note= "contains introns"
739..811
7499..81
1134..1186
/*tag= c
                                                                                                                          Location/Qualifiers
1..1929
                BP.
                AAZ58382 standard; DNA; 1929
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                                                 23-MAY-2000 (first entry)
                                                                                                          Exophiala spinifera.
                                                                                                                                                                                                     WO200004159-A1
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21-MAY-1999;
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                                 AAZ58382;
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RESULT 1
        AAZ58382
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The present sequence is that of an isolated nucleic acid, designated ESP002_C2, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAD, see AAPS8900) capable of degrading fumonishin, its Mydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycelial DNA using primers based on APAO of E. Spinifera ATCC 74269. The invention provides ARAD polynucleotides (see AAZS8383-87) and polypeptides (see AAYS8900-05) of E. Spinifera and Finnocladicals atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO enzyme in prokaryotic and non-plant enkaryotic producing APAO enzyme in prokaryotic and non-plant enkaryotic systems. Transgenic plants capable of degrading fumonisin or of graducing the degrading enzymes are provided. Methods for systems. Transgenic plants capable of degrading fumonisin or of elecontification of granin, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
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                                                                                                                                                                         New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
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Pred. No. 0;
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Best Local Similarity 100.0%;
Matches 1929; Conservative 0
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                                                                          Gilliam JT,
                                     (CURA-) CURAGEN CORP.
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The present sequence is that of an isolated nucleic acid, designated ESP002_C3, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58901) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycelial DNA using primers based on APAO of E. spinifera AACS 44269. The invention provides APAO polynucleotides (see AAX583183-87) and polypeptides (see AAX58900-05) of E. spinifera and ENINOCIDATE atrovitens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for systems. Transgenic plants capable of degrading fumonisin or of cetoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino polyol amine oxidase, fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
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1741 GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800
                                                                                     The present sequence is that of an isolated nucleic acid, designated ESP003_C12, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58902) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP003 mycelial DNA using primers based on AAPO of E. spinifera AAC58383-87) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the
                                                                                                                                                                                                                                                                                                           Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
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                                      GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA
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The present sequence is that of an isolated nucleic acid, designated RAT011-C2, of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see AAY58904) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO polymucleotides (see AAX58383-87) and polypeptides (see AAX58900-05) of R. atrovirens and Exophiala spinifera. The polymucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing
                                                                                                                                                      Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                                                                                         Rhinocladiella atrovirens amino polyol amine oxidase RAT011-C2 DNA.
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Best Local Similarity

Query Match

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detoxification; animal feed; silage; selectable marker;
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P-PSDB; AAY58905.
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The present sequence is that of an isolated nucleic acid, cheating and all of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see AAYS8905) capable of degrading fumonisin, its hydrolysis product API, and catated mycotoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO of E. spinifers ATC 74269. The invention provides APAO polynucleotides (see CAAS8838787) and polypeptides (see AAYS8900-05) of R. atrovirens and Exophiala spinifera. The polynucleotides are used to transformed plant cells normally susceptible to Fusarium or other toxin-producing transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-escrace in a transgenic plant, and for producing APAO encoming a transgenic plant, and for producing APAO encourse.
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Rhinocladiella atrovirens.
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silage; selectable marker; ds.
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GGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCGCCGTGTTCCGA
        TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGGCAATGG
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                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of an isolated nucleic acid, designated RAT011-C1, of Rhinocladiella atrovirens isolate RAT011, which encodes an amino polyol amine oxidase (APAO, see ARY58903) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of RAT011 mycelial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAT58938-87) and polypeptides (see AAY58900-05) of R. atrovirens and Exophiala spinifera. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing tungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-esterase in a transgenic plant, and for systems. Transgenic plants can hon-plant eukaryotic systems. Transgenic plants capable of degrading fumonish or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO plynucleotide is also useful as a selectable marker.
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Pred. No. 0;
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                                                                                                                                                                                          Maddox JR;
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                                                                                                                                                                                                                                                                      New isolated polynucleotides,
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21-MAY-1999;
                                                             08-JUL-1999;
                               27-JAN-2000
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                                                                                               1679
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                                                                                                                                                                                                      1920
                                                                                                                                                                                eed polynucleotides, polypeptides useful for detecting and fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA
                                                                                                                             GTCCCAGAGCCGGCCAACGTGCTCGAGTCGAGTGGTCGAAGCAGCAGTATTTCCAAGGA
                                                                                                                                                                                                     GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCCTAGCCTGGTGCCA
                                                   TCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG
                                                                                GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
                                                                                        GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG
                                                                                                                                                                        CCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG
                     TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG
                                                                                                                                                                                                                                                                                                                                  Exophiala spinifera amino polyol amine oxidase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 97-100; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maddox JR
                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HI-BRED INT INC
                                                                                                                                                                                                                                                                                      AAZ58402 standard; cDNA; 1803
                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US15454
                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0092936
                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0135391
                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       Exophiala spinifera.
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                                                                                                                                                                                                                                                 1920 GCAGCATAG 1928
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21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duvick JP,
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The present sequence is that of the coding region of full-length amino polyol amine oxidase (APAO) CDNA of Exophiala spinifera 2141.10. APAO is capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The invention provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAX58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be reconsisted from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonishin-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading con-plant eukaryotic systems. Transgenic plants capable of degrading (Monohish for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide is also useful as a selectable marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1602.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity 91.7%;
Matches 1769; Conservative
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1675 CCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG 1734
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P-PSDB; AAY68849
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Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding a full length aminopolyol amine oxidase APAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineered bacteria and fungi, e.g. rumen microflora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilliam JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1602.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 99-101; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..1803
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folkerts O,
                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                       AAZ60641 standard; DNA; 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.1%;
Best Local Similarity 91.7%;
Matches 1769; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US15455
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/product='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Tue Nov 12 09:29:59 2002

ATGGCACTTGCACCGAGCTACATCCCCCAAACGTCGCCTCCCCAGCAGGGTATTCC
TACATCGTCGACTACGCCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTAC 
TTTGCCCTTGACAGGCTCCCTCGTGCACGCTGGTGCCAGTACCGGCCTTGGC 
GAATACCTCTTTGAGGTTGATGCCACGGCCTGGTGCCAGGACACTCGACCCCAGACAC 
GTTGCGGACGTGGTAGTGGCGCCTGGCTTGAGCGGTTTGGAGACGGCAC 
CAGGCCGCGGTCTGTCCTGCCTCGTTCTTGAGGCGATGGATCGTGTAGGGGGAAAGACT 
CTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGGGCTGCGT 
AATGACAGCAACCAAGGGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGCGA 
CTCCAGAGGACGACGGGAAATTCAATCCATCAAGCACAAGACGGTACAACCACTACAGCT 
CTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 
AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGAGTTGCAAGTGCACTTGC
GGAACTCCTCCCGTAIGGTCTCAGCTGATCGAAGAGIAIAGCCTTGAAGACCCCAAGGC 
GAGCCCTCAGGCGAAGCGGCTCCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 
AAACTIGCCIGCTGTICTCAGCGIGGCAAACCAGAICACACGCGCTCIGCIGGGGGGGGGG
AGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGGTCTCAG

Qy Db	1081	TAATATTGTCTCGGACAAGAAGACGGCGGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140 
Qy	1141	ATGCAGTC
qq	1058	STATGCAGTCG
Q <sub>Y</sub> Db	1201	IGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCCGTCGCT 1260
ΟY	1261	TGAGCAGTCGGCGTCGTATAGTACGATCGGCCTCGGGCCCGTGTTCCG
qq	1135	GAAATTGAGCAGTCGGCATCCGGCTGTACAGTACGATCGGCCTCGGGCGCCGTGTTCCGA 1194
Qy	1321	AGCAAAAAGGIGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCA 1380
qa	1195	SAAAAAGGTGGTTTCGTTACCGACAACCTTGTATCCCACCTTGACATTTTCACC
δλ	38	
qa	1255	CTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAATTCTATCCTGGGCTACTATAG
Qy	1441	ATAGICITCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCITCTCGGGCGTCCTCCAA 1500 
QY	1501	TCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGC
qq	1375	TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGACGTCGACACTGCACAATGG 1434
δδ	1561	TCCATTACCTGTTTCATGGTCGGAGCCCGGGAGGGAGGGTGCTCCCAACAGTCCAAGGGG 1620
qq	1435	CATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTC
8	1621	68
3 8	i ac	** A A A C C C C C C C C C C C C C C C C
qq	55	61.
QY	1741	SCTGAACGATCTCACACTGGGGTTCGGCGCTCAGAAC
Db	1615	GAGCGCCGTC
oy q	0 1	86
gra Gra	C/9T	GGTTCAAGAGTGTTCGTTGGAACGGAGGCGTCTTTAGTTTGGAAAGGGTATATG 1
Qy Db	1861	GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920 
QY	1921	CAGCATAG 192
qq	1795	
RESU AAZ5 ID	LT 9 8407 AAZ58	1407 standard; cDNA; 2490 BP.
Y Y	AAZ58	407;
YY LO	23-MA	.Y-2000 (first entry)
DE	DNA e	ncoding GST-truncated
KW	Amino	<pre>polyol amine oxidase; APAO; fumonisin; mycotoxin; genic plant; detoxification; animal feed; silage;</pre>

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The present sequence is that of a polynucleotide encoding a GST.APAO fusion protein (see AAY58918) composed of glutathione S transferase and Exophiala spinifera amino polyol amino oxidase (APAO). 2 Codons of the APAO coding region have been altered by site-directed mutagenesis in order to change the glycosylation stren of the fusion protein. These were the replacement of AAT (Asn) by TCC (Ser) at codon 430, and replacement of AAT (Asn) at codon 435. APAO is capable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides can and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other coxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant cukaryotic systems. Methods for detecxification of grain, grain processing, silage, food crops and in animal feed and rumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting and in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2490;
   SS
selectable marker; glutathione S transferase; GST; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides, polypeptides useful for degrading fumonisin or structurally related mycotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2490 BP; 625 A; 623 C; 653 G; 589 T; 0 other;
                                                                                                                                "gst fusion + polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1596.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; Page 131-135; 154pp; English
                                                                                                                                                                                                       /*tag= c
/note= "extra lysine"
replace(1288..1290, TCC)
                                                                                                                                                                                                                                                                 replace(1303..1305, AAC)
                                                                                                                             /product= "gst fusion
688.2076
/*tag= b
/product= "K:trAPAO"
                                                                               Location/Qualifiers
1..687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         processing, silage, food crops and
microorganisms are also disclosed.
                           Chimeric - Schistosoma japonicum.
Chimeric - Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
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ilarity 91.5%;
Conservative
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                                                                                                                                                                                         688..690
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P-PSDB; AAY58918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degrading fumonisin
grain or in silage
                                                                                                                                                                                                                                                                                                           WO200004159-A1
                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998;
21-MAY-1999;
                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                        27-JAN-2000
                                                                                                                                              mat_peptide
                                                                                                     sig_peptide
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                                                        Synthetic.
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                                                                                                                                                                                                                                    mutation
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                                                                                                 TACATCGTCGACTACGCCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300
                                                                                                                                                  TITGCCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCTTGGCTTCACCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1455 GGAACTCCCCCGTATGGTCTCAGCTGATCGAAGACATAGCCTTCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1575 AAACTTGCCTGCTGTTCTCGGCGTAGCAAACCAGAICACACGCGCTCTGCTCGGTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 AGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGGTCTCAG
                                                                                                                                                                                                                                                                                                                                                         CTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                          601 AATGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAGAGGACGACCGGAAATTCAATCCATCAAGCACAAGACGGTACAACCACTACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 CCTTATGGTGACTCCCCGGTAAGCACACTCCCACTTTGTGATGAGACCTCTGTCGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1408 CCTTATGGTGACTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 GGAACTCCTCCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT
                       GACGCTTCGGGCGTGACAGACCCTGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT
                                               CTGCGAGCTTGCCTTGCTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC
                                                             GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCCCAGACAAC
                                                                                                                                                                                                                                                       GITGCGGACGTGGTAGTGGTGGCCTGGCTTGAGCGGTTTGGAGACGCCACGCAAAGTC
                                                                                                                                                                                                                                                                                                       CAGGCCGCCGGTCTGTCCTGCTTCTTGAGGCGATGGATCGTGTAGGGGGAAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGCAAGTGCACTTGC
GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCCAAGCATTCGCCAAT
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38; Indels 126;

61 CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

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1 ATGGCACTIGCACCGAGCTACATCAATCCCCCAAACGTCGCCTCCCCAGCAGGGTATTCC 60

; 0

Similarity

Best Local Sim Matches 1765;

us-09-771-045a-35\_1.rng

"GST/aminopolyol amine oxidase fusion"

misc\_feature

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       CAGGTATGCAGTCGATT 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2422 GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGGCTAGCCTGGTGCCA 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amine oxidase; APAO; mycotoxin degradation; antimicrobial; l invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                               GGAATTGAGCAGTCGGCTCTGTATAGTACGATCGGCCTCGGGCGCCGTGTTCCGA
                                                                                                                                                                                AGCAAAAAGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCA
                                                                                                                                                                                                   ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
                                                                                                                                                                                                                                                                                                                                                1561 TCCATTACCTGTTTCATGGTCGGAGCCGGGACGGAAGTGGTCCCAACAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2302 GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG
                                      TGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCCGGTCGCT
                                                                                                                                                                                                                                                       CCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                   TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGCAGTATTTCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a fusion of GST/mutated aminopolyol amine oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Exophiala spinifera.
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The present sequence encodes a fusion protein of GST and a mutated Exophiala spinifera aminopolyol amine oxidase (APAO). The APAO protein has been mutated to remove potential glycosylation sites at postions 201 and 206. The APAO enzyme has homology to the flavin contraining amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Contrainting or mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins has APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants of peroxide which is itself an antimicrobial and stimulates the plants of plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins con polypeptides is as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides or used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
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                                                                                                                                                                                                the protein has been mutated to remove potential glycosylation sites at positions 201 and 206"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
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Best Local Similarity 91.5
Matches 1765; Conservative
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P-PSDB; AAY68854.
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Db 1882 AGCAAAAAGGTGGTGGTTTCGTTACCGACCTTGTATCCCACCTTGACA 1941	QY       1381       CCTCTTCCGGCGGAAGCAACGGTTGGCGGAAAATCTATCCTCGGCTACTATAGCAAG       1440         D	OY 1441 ATAGTCTTCGTATGGGACAACCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCAA 1500 1611	OY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGG 1560	QY 1561 TCCATTACCTGTTCATGGTCGGGACCGGGACGGAAGTGGTCCCAACAGTCCAAGCAG 1620	OY 1621 GTACGACAAAGTCTGTGGGACCAACTCCGGGCAGCTACGAGAACGCCGGGGCCCAA 1680	QY         1681         GTCCCAGAGCCGGCCAACGTGCTCGAATCGAGTCGAAGCAGCAGTATTTCCAAGGA         1740           D         2242         GTCCCAGAGCCGGCCAACGTGCTCGAATCGAGTGGATCGAAGCAGCAGTATTTCCAAGGA         2301	OY 1741 GCTCCGAGGGCCGTCTATGGGCTGAACGATCTCATCACACTGGCTTCGGCTCAGAACG 1800	QY 1801 CCGTTCAAGTGTGTACATTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGTATAG 1860 	QY 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920	Qy 1921 GCAGCATAG 1929            	RESULT 11 AA258393 ID AA258393 standard; cDNA; 1442 BP.	XX AC AAZ58393; XX DT 23-MAY-2000 (first entry)			FH Key Location/Qualifiers FT CDS 11442 FT /*tage a /*t	FT intron 647699 FT XX XX WO200004159-a1	27-JAN-2000.	PF 08-JUL-1999; 99WO-US15454. XX DP 15-JTH-1008. 08HG-00008
241 TACATCGTCGACTACGCCCCGAGCAAACTCACACATTGGAGATGGGCTGAAGTCTACC 300 	CACCT					AATGACAGCAACCAAAGGGAAGTATCCAGATTGTTGAAAGATTCATTTGAGGCGAG					901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960 	961 AAACTTGCCTGTTCTCAGCGTGGCAAACCAGATCACAGGGGTTTGCTCGGTGTGGA 1020 	1021 AGCCCACGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCCACCGGTCTCAG 1080 	1081 TAATATTGTCTCGGAAAAAAAAGACGGGGGAGATATATGCGATGCAAAACAGGTGCGTG 1140 	CGATT	TCGCT	TCCGA	AGCAAAAAGGTGGTGTTCGTTACGACAACATGTATGTATG

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AAZ60631 standard; DNA; 1442
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                                                                                                                                                                                                                                                     The present sequence is that of polynucleotide k0n0-395_5.4, which encodes a truncated, but still functional, amino polyol amine oxidase (trApko-1, see AAY58907 and AAY58908). The polynucleotide was obtained by 3' and 5' RACE PCR using k0n0-395.5 (see AA258388), a partial APAO CDNA of Exphiala spinifera. APAO is capable of degrading fumonisin, its hydrolysis product API and related myxocxins. The invention provides APAO polynucleotides (see AA258383-87) and polypeptides (see AA258900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for expressing APAO in transgenic plants, animal feed and rumen microorganisms are also disclosed. APAO and in animal feed and rumen microorganisms are also disclosed.
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                                                                                                                                                              detecting and in processed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.4%; Score 1319; DB 21; Length 1442; 93.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide can also be used as a selectable marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                                                              ted polynucleotides, polypeptides useful for fumonisin or structurally related mycotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                          Example 6; Page 77-79; 154pp; English
                                                                                Maddox JR
                                 (PION-) PIONEER HI-BRED INT INC
 99US-0135391
                                                                                                             WPI; 2000-182425/16.
P-PSDB; AAY58907, AAY58908
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Matches 1417; Conservative
                                                                               Duvick JP, Gilliam JT,
                                                CORP
                                                                                                                                                                                            grain or in silage
                                                CURAGEN
                                                                                                                                                              New isolated degrading fum
21-MAY-1999;
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                                                                                                              1075 TCTCAGTAATATTGTCTCGGACAAGAAGACGGCGGGCAGTATATGCGATGCAAAACAGG
                                                                                                                                                                                                                                                                                                                                                    TCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCCC
                                                                                                                                                                                                                                                                                                                                                                           708 TCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAACACCCC
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                       TGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGCCACCGG
                                                                                                                                                                                                                     588 TCTCAGTAATATTTCTCGGACAAGAAGACGGCGGGCAGTATGTGCGATATGAAACAGG
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungithat produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related account of the organisms. The APAO polypeptides are used to
                                                                                              Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
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                                                                     DNA encoding an aminopolyol amine oxidase clone trAPAO-I.
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                                                                                                                                                                                                              "aminopolyol amine oxidase"
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                                                                                                                                                                                                                          /note= "contains an intron"
1..646
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                                                                                                                                                                        Location/Qualifiers
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647..699
/*tag= c
/number= 1
700..1439
/*tag= d
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/*tag= a
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                                                                                                                                            Exophiala spinifera.
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93.5%;
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                                                   AAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCG
                                                                                                       TGGATCAATGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAG
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                                                                        1188 GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTCGAGCAGCAGCAGTATTC
                                                                                                                                                                      1368 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAACCTG
CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC
         AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                              TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                  DNA encoding fumonisin esterase-amino polyol amine oxidase fusion.
                                AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                               GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                               CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                        Amino polyol amine oxidase; APAO; fumonisin esterase; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; barley; alpha-amylase; signal peptide; maize;
                                                                                                                                                                                                                                                                                                                                                                                                          /product= "barley alpha-amylase signal peptide'
73..2973
                                                                                                                                                                                                                                                                                                                                                                                                                                        "fumonisin-esterase-K:trAPAO fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "extra lysine codon"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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    Bacterium.
    Exophiala spinifera.

                                                                                                                                                                                                                                                     AA258404 standard; cDNA; 2976
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/product= '
73..75
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/*tag= a
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21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                Chimeric
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The present sequence is that of a polynucleotide encoding a fusion protein (see AAYS8915) composed of the barley alpha-amylase signal peptide, and a bacterial fumonisin esterase (BEST1) joined via a peptide linker to K:trAPAO (see AAYS8909), a truncated, but functional, amino polyol amino exidase of Exophiala spinifera. The construct was designed for expression and secretion in plants of a hybrid protein having BEST1 and AAPO activity. The invention provides AAPO polynucleotides (see AAZS883*87) and polypeptides (see AAYS8900-05) of E. spinifera and Rhinocladiella atrovirens. The conscription of Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing AAPO, optionally as a consistent with fumosinin esterase, in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for expressing characterial plants, in animal feed and rumen microorganisms are also disclosed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                             ed polynucleotides, polypeptides useful for detecting and fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1989 AGACCTCAAGGCGGACCCTCAGGCGAAGCGGCTCGACGAGTGTGAGCTTCGCGCACTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 GGGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                649 TTGGAGGGGGAGCTCCAGAGGACGACCGGAAATTCAATCCATCAAGCACAAAGACGGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2976 BP; 564 A; 932 C; 926 G; 554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.8%; Score 1212.2;
ilarity 90.2%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                         Example 13; Page 109-113; 154pp; English
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Matches 1372; Conserv
                                                                                                                                                    grain or in silage
                               P-PSDB; AAY58915
                                                                                         New isolated
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Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;

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1488
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                                                                                                                                                                                                                                                                                                             GCTCGGTGTGGAAGCCCACGAGATCAGCATGCTTTTTTCTCACCGACTACATCAAGAGTGC
                                         ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
                                                                                                                                                                            GCCGTGTTCCGAAGCAAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTG
                                                                                                                                                                                                                                                                     GATCGGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA
                                                                          AACAGGTGCGTGCGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT
                                                                                                 T----CAGGT
                                                                                                                                             ATGCAGTCGATTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACCTCAAC
                                                                                                                                                                  ACCCCCGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCTCGGGC
                               CACCGGTCTCAGTAATATTGTCTCGGACAAGAAGACGGCGGCGGCAGTATATGCGATGCAA
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                                                                                                   AA----
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The present sequence encodes a fusion protein of Exophiala spinifera aminopolyol amine oxidase (APAO) and a bacterial fumonisin esterase. The APAO enryme has homilology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other plant materials, including expression in engineered bacteria and fungi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels 126;
                                                                                                                                                   oxidase/fumonisin
                                                                                                                                                                                                                                                                                                                                                           /note= "the protein has an amino terminal Lys for optimized expression"
                                                                                                                                                                                                       /note= "barley alpha amylase signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aminopolyol amine oxidase, used, to Fusarium -
                       plant fungal invasion; hydrogen peroxide; Fusarium; fungl; fumonisin esterase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maddox
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                                                                                                                                                                                                                                                                                                                                              "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilliam JT,
                                                                                                                                                                                                                                               "fumonisin esterase"
                                                                                                                                                   "aminopolyol amine
                                                                                                                                                                                                                                                              /note= "bacterial fumonisin
                                                                                                                                                                esterase fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1212.2;
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0; Mismatches
                                                                                                                                                                                                                                                                                                     /noté= "spacer sequence"
1585..2973
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                                                                                                          Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.8%;
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                                                                                                                                                                                                                                  /product= "
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/product=
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generate plants resistant
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                                                                                                                                                   /product=
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Best Local Similarity 90.2
Matches 1372; Conservative
                                                                                                                                                                                                                     73..1545
                                                                                                                         .2976
                                                                                                                                                                                           /*tag=
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                                                                  Synthetic.
Exophiala spinifera.
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                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                       mat_peptide
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                                                                                                            Key
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DNA encoding a fusion of aminopolyol amine oxidase/fumonisin esterase.

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ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAA 1608
                                                       CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAAC 1668
                                                                                                                                                  CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAG 1728
                                                                                                                                                                                                      CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCG 1788
                                                                                                                                                                                                                                                           GGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCT 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .n esterase-amino polyol amine oxidase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kidase; APAO; fumonisin esterase; mycotoxin;
toxification; animal feed; silage;
arley; alpha-amylase; signal peptide; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1- a
luct= "barley alpha-amylase signal peptide"
8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uct= "fumonisin-esterase-K:trAPAO fusion"
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"extra lysine codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NA; 3003 BP
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|CATAG 2976
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Spinifera.
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The present sequence is that of a polynucleotide encoding a fusion protein (see AAY58914) composed of the barley alpha-amylase signal peptide, and Exophiala spinifera fumonistin esterase (ESP1) joined via a peptide linker to K:trAPAO (see AAY58909), a truncated, but functional, amino polyol maine oxidase of E. spinifera. The construct was designed for expression and secretion in plants of a hybrid protein having ESP1 and APAO activity. The invention provides APAO polynucleotides (see AAX58383*87) and polypeptides (see AAX58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO, optionally as a conscient with fumosinin esterase, in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2015
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                                                                         detecting and in processed
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1729 GGGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTCGAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCACTACAGCTCCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 ACCCCAGACAACGTTGCGGACGTGGTAGTGGTGGCCGCTGGCTTGAGCGGTTTGGAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGAAAGACTCTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.8%; Score 1212.2; DB 21; Length 3003; llarity 90.2%; Pred. No. 0; Conservative 0; Mismatches 23; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3003 BP; 690 A; 840 C; 819 G; 654 T; 0 other;
                                                                        ted polynucleotides, polypeptides useful for fumonisin or structurally related mycotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Page 102-106; 154pp; English
 Maddox JR;
 JI,
Gilliam
                            2000-182425/16
                                                                                                          in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                             P-PSDB; AAY58914
                                                                           isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim
Matches 1372;
 JP,
                                                                                          degrading
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                          grain or
 Duvick
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                                                       GCCGTGTTCCGAAGCAAAAAGGTGGTGTTTCGTTACCGACAACATTGTATCCCACCTTG
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           CACCGGTCTCAGTAATATTGTCTCGGACAAGAAGACGGCGGCGGCAGTATATGCGATGCAA
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729 bp mRNA linear EST 08-MAR-2002
BJ375584 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc19a09 3', mRNA sequence.
BJ375584
BJ375584.1 GI:19284967
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 729)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contect: Tadasu Shin-i
Contect For Genetic Senetics
Illi Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 729
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/strain="XXX"
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BJ375460
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BJ341279 BJ341279
BJ373006 BJ373006
BJ377633 BJ377633
BJ431313 BJ431313
BJ374786 BJ374786
                                            2002, 02:21:50 ; Search time 2809 Seconds (without alignments) 11121.785 Million cell updates/sec
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      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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BJ429162 BJ375168 BJ398900 BJ430839 BJ374842

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1 (bases 1 to 742)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                  1244 TCAACACCCCGTCGCTGGAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCT 1303
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                                                                                                         0; Mismatches 362;
                                                                              3.0%; Score 58.8; DB 13; 44.3%; Pred. No. 1.5e-05;
                      /dev_stage="Culmination stage"
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1304 CGGCCCCGTGTTCCGAAGCAAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCA 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1664 AGAACGCCGGGGCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGC 1723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 ATGACGATAAGAAAACAGCTATCGTTGGTTTCATTGCTGCTTCAGCCGCTAAAGATTGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 AAGAATATTCACGTGGTTGTTATTTAGGTTACACTAGTCCAGGTACTCTTACCAATGTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/clone_lib="Dictyostelium discoideum cDNA library,
/sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1424 TCGGCTACTATAGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCT
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                 Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
Tal: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@enes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                          discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.0%; Score 58.8; DB 13;
14.3%; Pred. No. 1.5e-05;
Lve 0; Mismatches 362;
                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Aggregation stage"
142 c 132 q 252 t
                                                                                                                                                                                                        1.742
/organism="Dictyostelium
/strain="AX4"
/db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.3%;
Unpublished (2002)
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ij

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124 GGTGCCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTAAAAGATA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57.4; DB 13;
Pred. No. 3.7e-05;
0; Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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141 c 130 g 243 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:44689"
/clone="ddc25101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                 BJ377633
BJ377633.1 GI:19287016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="AX4"
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ilarity 44.9%;
Conservative
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Matches 263;
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                                                                                                           RESULT 4
BJ377633/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                          AUTHORS
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                  08-MAR-2002
                                   Dictyostelium
                                                                                                                                                                                                                    culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="ddc15e09"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1384 CTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGGTCCAAGGGGTA 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAAGTC 1683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGTTGGTTTCATTGCTGCTTCAGCCGCTAAAGATTGGGCTGAAAAATCACCAGAAGAA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AGAAAGAGGCCGTCTTAGACTGTTATGCTCGTTGGT------GGGGTCCAAAAGCA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                       Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 711)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the
                  BJ373006 Dictyostelium discoideum cDNA library, CF discoideum cDNA clone ddc15e09 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                    1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshinigenes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 57.8; DB 13;
45.1%; Pred. No. 2.8e-05;
tive 0; Mismatches 313;
                                                                                                                                                                                                                                                                    Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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130 c 121 g 240 t
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                                                                    BJ373006
BJ373006.1 GI:19282389
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="AX4"
                                                                                                                                                                                                                                                   Unpublished (2002)
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BJ373006/c
LOCUS
                                   DEFINITION
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                                                                                                                                                                                               AUTHORS
TITLE
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                                                                      ACCESSION
                                                                                     VERSION
KEYWORDS
SOURCE
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EST 08-MAR-2002
Dictyostelium
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 730)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-1, T.
Full length cDNA of Dictyostelium discoideum at the culmination
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184 GTTGGTAGAATTCATTGGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTTATATGGAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                      BJ377633 Dictyostelium discoideum cDNA linear discoideum cDNA library, CF discoideum cDNA clone ddc25101 3', mRNA sequence.
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BJ431313 Dictyostelium discoideum cDNA library, VF Dictyostelium
discoideum cDNA clone ddv13p15 3', mRNA sequence.
                               1744 CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACGCCG 1803
                                                                                            1804 TICAAGIGIGITCATITCGTIGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATGGAA 1863
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 610)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.,
Full length cDNA of Dictyostelium discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Dictyostellum discoideum cDNA library, VF"
/sex="mat A"
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                                                   200 TATTTAGGTTACACTAGTCCAGGTACTCTACCAATGTGGTGAACATTNACGTGCTCCA 141
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                                                                                                                                                                               /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57.2; DB 13;
Pred. No. 3.8e-05;
0; Mismatches 309;
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122 c 107 g 201
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Location/Qualifiers
1. .610
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BJ374786 BJCtyostellum discoideum cDNA library, CF Dictyostellum discoideum cDNA library, CF Dictyostellum discoideum cDNA clone ddc16407 3', mRNA sequence.
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1 (bases 1 to 611)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-1, T.
Full length cDNA of Dictyostellum discoldeum at the culmination
                                                                                                                                                                                                                                                  1744 CCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACGCCG 1803
1624 CGACAAAAGICIGICIGGGACCAACICCGCGCAGCCIACGAGAACGCCGGGGCCCAAGIC 1683
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/sex="mat A"
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                                                                                                                                                                                                                                                                                                                                                                                                              139 GTTGGTAGAATTCATTGGCTGGTACAGAAACTGCTTCAGTTTGGATTGGTTATATGGAA
                                                          310 AGAAAGAGAGCCGTCTTAGACTGTTATGCTCGTTGGT------GGGGTCCAAAAGCA
                                                                                                                           1684 CCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAGGAGCT
                                                                                                                                                                                  259 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAAGAAGAAGAAGAATATTCACGTGGTTGT
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Contact: Tadasus Shin-i
Contact: Tadasus Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6855
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ilarity 45.1%; Pred. No. 3.8e-05;
Conservative 0; Mismatches 313;
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125 c 113 g 192 t
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/db_xref="taxon:44689"
/clone="ddc16d07"
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Location/Qualifiers
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Dictyostelium discoideum
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Eukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.

Eukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.

1 (bases 1 to 635)

5 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the slug stage
Unpublished (2002)

Contact: Tadasu Shin-i
Enail: Cantachin-i
Location/Qualifiers
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                                                             GTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGGCGTCCTCCAATCG 1503
                                                                                                                                               1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGGTCC 1563
                                                                                                                                                                                                                                ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGGCAGGTA 1623
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                                                                                                                                                                                                                                                          180 TATITAGGITACACTAGICCAGGIACTCICIACCAAIGIGGIGAACAITIACGIGCICCA 121
                                                                                                     471 ATCACCATCTATGATGAACCATTCTGGAGAAAAGAAGGTTATTCAGCTGAAGCCATCTCT 412
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                                                                                                                                                                                                                                                                                                                                                     291 AGAAAGAGCCGTCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGA
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                                                                                                                                                                                      GATAAAGGTCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT
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Pred. No. 3.9e-05;
0; Mismatches 313;
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125 c 112 g 2
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/clone="dds5f18"
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Dictyostelium discoideum
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BJ399347/C
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 612)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the vegetative
  1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGGCAATGGTCC 1563
                                                                                   ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCCAAGCAGGTA 1623
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                                                                                                              181 TATTTAGGTTACACTAGTCCAGGTACTCTACCAATGTGGTGAACATTTACGTGCTCCA 122
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                            412 GATAAAGGTCCAATCTTTTATCTGCTATGATGACTCTTCACATGATGACAGCT
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Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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/organism="Dictyostelium discoideum"
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Pred. No. 3.8e-05;
0; Mismatches 313;
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125 c 113 g 194
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/clone="ddv1j21"
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                           CTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAGATA 1443
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1 (bases 1 to 648)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the culmination
 AAAAAGGTGGTGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCACCT 1383
                                                                                                                          GICTICGIAIGGGACAACCCGIGGIGGCGCGAACAAGGCIICICGGGCGICCICCAAICG 1503
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                                                                                  557 ATGCCACCAAGACGTGATGAACTCACTCAAAGAATGCCAATGGGTTCCGTCATAAAACC 498
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/clone="ddc18m13"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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                497 ATCACCATCTATGATGAACCATTCTGGAGAAAGAAGGTTATTCAGCTGAAGCCATCTCT
                                                                                                                                                                                                                                                1564 ATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCAAGCAGGTA
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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Location/Qualifiers
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Dictyostelium discoideum
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BJ375565 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc19m05 3', mRNA sequence.
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

I (bases 1 to 650)

Grushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the culmination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 ATGCCACCAAGACGTGATGAACTCAACTAAAGAATGCCAATGGGTTCCGTCATTAAAACC 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 GATAAAGGICCAATCTITAICTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 ITAICICCAAGAAICTITITAGAGAAAGITGGAAAGAAGAAGAATAITCACGIGGTIGI 216
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                                                                                                                                                                                                          Gaps
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                                                                                                                                       Length 648;
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                Score 57.2; DB 13;
Pred. No. 3.9e-05;
0; Mismatches 313;
/dev_stage="Culmination stage" a 125 c 114 g 217 t
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Center For Genetic Resource Information
National Institute of Genetics
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Location/Qualifiers
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BJ375565.1 GI:19284948
                                                                                                                            3.0%;
ilarity 45.1%;
Conservative
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Gaps

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BJ430839 658 bp mRNA linear EST 13-MAR-2002 BJ430839 Dictyostelium discoideum cDNA library, VF Dictyostelium discoideum cDNA clone ddv9b03 3', mRNA sequence.
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                                                                                                                                                                               /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc11k04"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1324 AAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCACCT 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GIIGGIAGAATICATIGGGCIGGIACAAACIGCTICAGIIIGGATIGGIIAATGGAA 104
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                                            Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 3.0%; Score 57.2; DB 13; Best Local Similarity 45.1%; Pred. No. 3.9e-05; Matches 264; Conservative 0; Mismatches 313;
                                                                                                                                                                                                                                                                                                                         /dev_stage="Culmination stage"
124 c 113 g 223 t
Center For Genetic Resource Information
National Institute of Genetics
                                       1111 Yata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tahiniqqenes.nig.ac.jp.
Location/Qualifiers
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BJ372067 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc11k04 3', mRNA sequence.
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Dictyostelium discoideum

Dictyostelium discoideum

Bukaryotis Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 651)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the culmination
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                   /organism="Dictyostelium discoideum"
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/clone="ddc19m05"
/clone_lb="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
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                                                                                                                                                      /dev_stage="Culmination stage"
124 c 113 a 221 t
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Contact: Tadasu Shin-i
                                                                                                                                                                                        192
                                                                                                                                                                                                                                                                                                          264:
                                                                                                                                                                                                                                                             Query Match
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BJ374842 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc16b17 3', mRNA sequence.
                                                                                                                                              Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 686)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
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                                                                                                                                                                                                                                Unpublished (2002)
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
Email: tshini@genes.niq.ac.in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.0%; Score 57.2; DB 13;
Similarity 44.1%; Pred. No. 4.1e-05;
04; Conservative 0; Mismatches 363;
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/db_xref="taxon:44689"
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Location/Qualifiers
                                                                                                          Dictyostelium discoideum.
Dictyostelium discoideum
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BJ374842.1 GI:19284225
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Matches 294;
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/db_xxref="taxon:44689"
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                                    Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
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1 (bases 1 to 658)
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3.0%; Score 57.2; DB 13; Length
Best Local Similarity 45.1%; Pred. No. 4e-05;
Matches 264; Conservative 0; Mismatches 313; Indels
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                                                                                         Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/dev_stage="Growth phase"
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/organism="Dictyostellum discoideum"
/Stran="AA"
/Gb_xref="taxon:44689"
/clone="ddv2f15"
/clone_lib="Dictyostellum discoideum cDNA library, VF"
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                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 687)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the vegetative
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GEGAACATITACGIGCICCAGITGGIAGAATICATICGCCIGGIACAGAAAACIGCITCAG 82
                                                                        81 TITGGATIGGITATATGGAAGGIGCCITAGAATCAGGITTIAGAGITTCAAAAGAAATTA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information
National Institute of Genetics
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/dev_stage="Growth phase"
135 c 129 g 221 t
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                           BJ429162.1 GI:19403884
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
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EST 08-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases I to 694)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin'i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
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                                                                                                                                                                     1664 AGAACGCCGGGGCCCCAAGTCCCAGACCCGGCCAACGTGCTCGAAATCGAGTGGTGGAGC 1723
                                                                                                                                                                                                                                                                              1724 AGCAGTATTTCCAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGG 1783
                                                                                                                                                                                                                                                                                                                                                                                          GTTCGGCGCTCAGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAG 1843
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/db_xref="taxon:44689"
/clone="dec17n18"
/clone_lib="Dictyostellum discoideum cDNA library, CF"
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372 ATGACGATAAGAAAACAGCTATCGTTGGTTTCATTGCTGCTTCAGCCGCTAAAGATTGGG 313
                                                                                                                                                                                                                                                                                                                                                                                                                        1604 CCCAACAGTCCAAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACG
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Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Eax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Pred. No. 4.1e-05;
0; Mismatches 313;
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132 c 126 g 233 t
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Location/Qualifiers
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1444 GICTICGIAFGGGACAACCCGFGGGGGGGGAACAAGGCTICTCGGGCGTCCTCCAAFCG 1503
             210 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCAATGTGGTGAACATTTACGTGCTCCA 151
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Sequence 41,
Sequence 22,
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-352-159-32

US-09-352-159-32

US-09-352-168-32

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US-09-352-168-16
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US-09-352-159-35

Sequence 35, Application US/09352159A

Patent No. 621434

Patent No. 6214434

CERNERAL INFORMATION:

APPLICANT: Duvick, Jonathan P.

APPLICANT: Maddox, Joyce R.

TITLE OF INVENTION: Amino Polyol Amine Oxidase

TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use

FILE REFERENCE: 134

CURRENT APPLICATION NUMBER: US/09/352,159A

CURRENT FILING DATE: 1999-07-12

EARLIER FILING DATE: 1999-07-25

EARLIER FILING DATE: 1999-07-25

EARLIER APPLICATION NUMBER: 60/092,336

EARLIER FILING DATE: 1999-07-25

EARLIER APPLICATION NUMBER: 60/0135,391

EARLIER FILING DATE: 1999-05-21

SOFTWARE: FastEQ for Windows Version 3.0

SSPTWARE: FastEQ for Windows Version 3.0
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Sequence 2, Appli
Sequence 3, Appli
Sequence 31, Appli
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Sequence 372, Appl
Sequence 15, Appl
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US-09-352-168-1

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US-09-352-168-1

US-09-352-168-2

US-09-230-388-2

US-09-230-388-2

US-09-428-517-1

US-08-132-168A-31

US-09-199-637A-374

US-09-199-637A-366

US-09-199-637A-1

US-09-199-637A-1

US-09-199-637A-1

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100.0%; Score 1929;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1929; Conservative 0; Mismatches
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ORGANISM: Exophiala spinifera
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LOCATION: (739)...(811)

NAME/KEY: intron

LOCATION: (1134)...(1186)

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Sequence 37, Application US/09352159A

Sequence 37, Application US/09352159A

GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
CURRENT APPLICATION NUMBER: US/09/352,159A

CURRENT FILING DATE: 1998-07-12

EARLIER PILING DATE: 1998-07-25

EARLIER FILING DATE: 1999-05-21

EARLIER PLICATION NUMBER: 60/135,391

EARLIER FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 3.0
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                                   ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
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NAMB/KEY: intron
LOCATION: (1134)...(1186)
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ORGANISM: Exophiala
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            Polypeptides
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TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Pol
FILE REFERENCE: 1134
FURRENT APPLICATION WUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER PILLING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NO 39
LENGTH: 1930
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                                                                                                                                                                                                                               96.0%; Score 1851.4; 97.8%; Pred. No. 0;
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                                                                                                                   TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
NAME/KEY: intron
LOCATION: (739)...(811)
NAME/KEY: intron
LOCATION: (1134)...(1187)
NAME/KEY: misc_feature
LOCATION: (648)...(648)
OTHER INFORMATION: n = A,T,C or
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Matches 1887; Conservative
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of TILE REPERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER PILING DATE: 1999-07-25
EARLIER PILING DATE: 1999-05-21
NUMBER: OF SEQ ID NOSE: 46
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                ITTGCCCTTGACAGGCTCCCTCCTTGCACGCTGCTGCCAGTACCGGCCTTGGCTTCACCT 360
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                               Sequence 43, Application US/09352159A Patent No. 6211434 GENERAL INFORMATION:
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95.98;
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Best Local Similarity 95.9
Matches 1850; Conservative
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LOCATION: (739)...(811)
NAME/KEY: Intron
LCCATION: (1134)...(1186)
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Sequence 45, Application US/09352159A

GENERAL INFORMATION:
APPLICANT: BUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynolectides and Related Polypeptides and Methin FILE OF INVENTION: Polynolectides and Related Polypeptides and Methin FOLKENT APPLICATION NUMBER: US/09/352,159A

CURRENT APPLICATION NUMBER: G0/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-07-12

EARLIER FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 46

SEQ ID NOS: 46

SEQ ID NO 45-06

SEQ ID NO 45-06

SEQ ID NO 45-06

SED AND 45
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95.8%; Pred. No. 0;
Live 0; Mismatches
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                                                                                                                                                       Score 1787.4;
Pred. No. 0;
0; Mismatches
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EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 41
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                                                                                                                                                                   Best Local Similarity 95.7
Matches 1847; Conservative
                                                                                           NAME/KEY: intron
; LOCATION: (739)...(811)
; NAME/KEY: intron
; LOCATION: (1134)...(1185)
US-09-352-159-41
                                                                          ORGANISM: Rhinocladiella
                                                                 TYPE: DNA
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                  CGGTGTCCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGTATGCAGTCGATT
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Patent No. 6211434
GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Pol;
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
CURRENT FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
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US-09-352-159-41
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GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Maddox, JOYCE R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyoucleotides and Related Polyer ELERERARY.
CURRENT APPLICATION NUMBER: 05/09/352,159A
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-07-12
SARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SEG ID NOS: 46
SEG ID NO 22
LENGTH: 1803
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Pred. No. 0;
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0; Mismatches
Sequence 22, Application US/09352159A Patent No. 6211434
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Patent No. 6211435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Crasta, Oswald R.
APPLICANT: Criteria, Osto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Poly
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-12
SERLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE FELLIAND AND SERVICES FALLIAND SERVICE
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0; Mismatches
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Best Local Similarity 91.7%;
Matches 1769; Conservative (
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-09-352-168-22
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEO ID NOS: 46
SEQ ID NOS: 46
SEQ ID NO 32
LENGTH: 2490
                                                               1255 CCTCTTCCCGCCGAGAAGCAAGCATGGCGGAAAATTCTATCCTGGGCTACTATAGCAAG 1314
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PENTURE:
OKGANISM: Unknown
PENTURE:
OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST
OTHER INFORMATION: and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;
OTHER INFORMATION: mutation in putative glycosylation sites, nt
PENTURE:
PENTURE:
                                              CCTCTTCCCGCCGAGAAGCAAGCATTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG
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; Sequence 32, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
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                                                                                                                                                          Score 1596.2;
Pred. No. 0;
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llarity 91.5%;
Conservative
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                                                                                           LOCATION: (1288)...(1290)
OTHER INFORMATION: mutation
FEATURE:
NAME/KEY: mutation
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NAME/KEY: CDS
LOCATION: (1)...(2487)
NAME/KEY: misc_feature
LOCATION: (1)...(687)
OTHER INFORMATION: GST and
FEATURE:
NAME/KEY: misc_feature
LOCATION: (688)...(2490)
OTHER INFORMATION: G1yc (-)
FEATURE:
NAME/KEY: misc_feature
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Best Local Simil
Matches 1765; (
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                                              AGAATACAGTCACTGCACTTCGTCCAGCTGAGCGAGGAGGTTGCAAGTGCACTTGC
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APPLICANT: DIVIGENTION:
APPLICANT: DIVIGENTS, Onathan P.
APPLICANT: DIVIGENTS, Onathan P.
APPLICANT: Folkerts, Orto
APPLICANT: Folkerts, Orto
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynclectides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 33
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OTHER INFORMATION: and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;
OTHER INFORMATION: mutation in putative glycosylation sites in bold
OTHER INFORMATION: mutation in putative glycosylation sites in bold
OTHER INFORMATION: 1303-1305 (AGC-> AAC).
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(687)
OTHER INFORMATION: GST and linker
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(687)
OTHER INFORMATION: GST and linker
FEATURE:
NAME/KEY: misc_feature
COCATION: (488)...(2490)
OTHER INFORMATION: G1yc (-) APAO
                           2422 GAAGGGCCATACGATCGGGTCAACGAGGTGCAGAAGTTGTGTGGCGTAGCCTGGTGCCA 2481
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; OTHER INFORMATION: mutation in putative glycosylation site (AGC->AAC)
US-09-352-168-32
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OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)
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            1861 GAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA
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                                                                                                                                                                   Sequence 32, Application US/09352168A Patent No. 6211435 GENERAL INFORMATION:
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                                                                                           Score 1319;
Pred. No. 0;
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93.5%;
        ; LOCATION: (1)...(646)
; NAME/KEY: intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-159-7
                                                                                                                   Conservative
                                                                                                        Similarity
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            GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA
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                                                                                                                                            ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA
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 GGAATTGAGCAGTCGGCGTGTATAGTACGATCGGCCTCGGGCGCCGTGTTCCGA
                                               AGCAAAAAGGTGGTGGTTTCGTTACCGACAATGTTGTATCCCACCTTGACATTTTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7. Application US/09352159A

Patent No. 6211434

GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Anino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Poly
FILE REFERENCE: 1134
FILE REFERENCE: 134
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER PILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFFWARE FASTENCE FASTENCE OF Windows Version 3.0
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                                                         DB
                                                                             Mismatches
                                                      Score 1319;
Pred. No. 0;
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0
                                                     68.4%;
93.5%;
                                                                           Matches 1417; Conservative
      ; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-168-7
                                                                 Similarity
                                                     Query Match
                                                                 Best Local
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Patent No. 6711435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Polketts, Otto
APPLICANT: Folketts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
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TTCCGAAGCAAAAGGTGGTGGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTT 1374
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                                                          CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGG
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NAME/KEY: intron
LOCATION: (647)...(699)
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                  Score 1212.2;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                   LOCATION: (1)...(2973)
NAME/KT: misc.leature
LOCATION: (1585)...(1587)
OTHER INFORMATION: Extra lysine
                         mature
                                                                                                                                                                                                                                                                                                    62.8%;
90.2%;
                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1585)...(2973)
OTHER INFORMATION: K:trAPAO
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                                                                    LOCATION: (1546)...(1584)
OTHER INFORMATION: spacer
OTHER INFORMATION: BEST1
FEATURE: MARZ/KEY: misc_feature
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(1546)...(158
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
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Best Local Simi
Matches 1372;
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TITLE OF INVENTION: Polyol Amine Oxidase
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT APPLICATION NUMBER: GO/092,936
EARLIER FILING DATE: 1999-07-15
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARRE: FASSEQ for Windows Version 3.0
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                                                                             948 AGCAAGATAGTCTTCCTATGGGACAAGCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTC
                                                                                                                        CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGG
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          AGCAAGATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGGACAAGGCTTCTCGGGCGTC
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OTHER INFORMATION: Barley alpha amylase signal sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09352159A
Patent No. 6211434
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                                                                          OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1 OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. ROTHER INFORMATION: plant expression.
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                                                                                                                                                                            alpha amylase signal sequence
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                                                                                                                                                                                                 NAMESKEY: mat_peptide
LOCATION: (73)...(1545)
OTHER INFORMATION: BEST1 mature
FEATURE:
FEATURE:
LOCATION: (1546)...(1584)
OTHER INFORMATION: Artificial spacer sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.8%; Score 1212.2;
90.2%; Pred. No. 0;
tive 0; Mismatches
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: NAME/KEY: misc_feature
: LOCATION: (1585)...(1587)
: OTHER INFORMATION: Extra lysine
US-09-352-168-26
                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1585)...(2973)
OTHER INFORMATION: K:traPAO
                                                                                                                                                      LOCATION: (1)...(72)
OTHER INFORMATION: Barley
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                           NAME/KEY: sig_peptide
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                               TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1)
SEQ ID NO 26
LENGTH: 2976
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Best Local Simi
Matches 1372;
                                                              FEATURE:
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Batent No. 6211435

GENERATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Calliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of USFILE REFERENCE: 0875
CURRENT FILING DATE: 1999-07-12
EARLIER PFLICATION NUMBER: 60/092,936
EARLIER PTLING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                    GCTCGGTGTGGAAGCCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTGC
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1129 AACAGGTGCGTGCGGTCTCTCAGGTAGGGGACTCGTTTCTTAGTGGTCATTCCAGGT
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyouclectides and Related Polypeptides and Methods of Uses
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                   Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACGCAAAGICCAGGCCGCCGGICTGICCTGCCTCGTTTGAGGCGATGGAICGIGIA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Sequence is barley alpha amylase signal sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       709 ACCACTACAGCTCCTTATGGTGACTCCCGGTAAGCACAATCCCACTTTGTGATGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6211434
OTHER INFORMATION: espl mat: an artificial spacer sequence
OTHER INFORMATION: K:trAPAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(72)
OTHER INFORMATION: Barley alpha amylase signal sequence FEATURE:
NAME.KER:
NAME.KER:
LOCATION: (73)...(1575)
OTHER INFORMATION: espl mat
FEATURE:
NAME.KER:
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Pred. No. 0;
0; Mismatches
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; LOCATION: (1612)...(1614)
; CTHER INFORMATION: Extra lysine
US-09-352-159-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.8%;
90.2%;
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NOAME/KEY: misc_feature
LOCATION: (1612)...(3000)
OTHER INFORMATION: K:trAPAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.2'
Matches 1372; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide LOCATION: (1)...(72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3003
TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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		TGCCATGCCAAAGGACTTTTTCCAGGGGGACTTGTTCCAGGGGGACTTGTTCCAGGGGACTTGTTCCAGGGGACTTGTTCCAGGGATCGGCTGTAAAGGACTTGTTCCAGGGAAAGGACTTGTTCCAGGAAAGGAAAGTTGTAAAGGAAAAGAAAG	CGTCCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGT
00 4 6 6 9 1 4 6 9 1	2076 TGA 1009 GCTK 2136 GCTK 1069 CACK 2196 CACK 1129 AACK 1129 AACK 1189 ATK	2263 ATI 1249 ATI 1309 GC 1309 GC 1369 ACI 1369 ACI 1369 ACI 1429 TAI 2503 TAI	1489 GGCC 1549 GATU 1549 GATU 1609 CAGT 1609 CAGT 1609 GCCC 1609 GCCC 1729 TATU 1729 TATU 1729 TATU 1789 GCGC 1789 GCGC
0 0 y		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. qq

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November 12, 2002, 03:21:40; Search time 140 Seconds (without alignments) 4888.437 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                             320260 seqs, 177392727 residues
                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                             US-09-771-045A-35
1929
                                                                                                                                               Title:
Perfect score:
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                                                            OM nucleic
                                                                                                                                                                            Sequence:
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                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

tion	nce 1583, Ap	nce 2391, Ap	-	nce 562, App		nce 3971, Ap	nce 2, Appli		nce 2388, Ap		86, 4	nce 376, App	nce 1744, Ap	۲,	٠.	nce 1008, Ap	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli
Description	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Sedne	Sedu	Sedu
D	US-09-954-456-1583	US-09-880-107-2391	US-09-917-800A-1612	US-09-925-301-562	US-09-974-300-239	US-09-960-352-3971	US-09-912-176-2	US-09-925-302-242	US-09-880-107-2388	US-09-925-300-617	US-10-044-090-86	US-09-925-301-376	US-09-880-107-1744	US-10-044-090-339	US-09-795-668-1008	US-09-795-686-1008	US-09-349-015-3	US-09-795-668-1	US-09-795-686-1
	10	10	10	10	10	10	10	10	10	10	12	10	10	12	10	10	10	10	10
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% Query Match	2.1	2.1	2.0	2.0	1.9	1.9	1.9	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8
Score	40.8	40.8	39	38	37.6	37.2	36.6	35.2	34.8	34.8	34.8	34	34	34	33.8	33.8	33.8	33.8	33.8
Result No.	1	7	m	Ω <b>4</b>	S	9	7	œ ن	6	10	11	12	13	14	15	16	17	18	19

Sequence 7, Appli Sequence 947, App Sequence 12, App Sequence 1765, Ap Sequence 1765, Ap Sequence 134, Ap Sequence 234, App Sequence 34, App Sequence 34, Appli Sequence 3, Appli Sequence 7, Appli Sequence 4052, Ap Sequence 283, Appli Sequence 283, Appli Sequence 15, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli	
US-09-904-065-7 US-09-728-446-947 US-09-560-863-412 US-09-974-298-80 US-09-980-107-1765 US-10-66-933-1599 US-09-867-1059-1599 US-09-867-17-149 US-09-799-777-149 US-09-799-777-149 US-09-925-299-234 US-09-925-299-234 US-09-915-289-7 US-09-815-242-4052 US-09-815-242-4052 US-09-815-242-4052 US-09-915-242-4052 US-09-904-065-5 US-09-904-065-5 US-09-861-289-3	US-09-803-589-5 US-09-815-24-9802 US-09-864-864-314 US-09-815-242-8018 US-09-756-186-3 US-09-764-878-391 US-09-764-878-391
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3708 413 3013 3015 443 463 22609 3141 1157 1157 116029 981 1140 3708	979 1428 2623 420 645 1202 442 579
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888 88884444444444	31.8 31.4 31.4 31.4 30.8
200 200 200 200 200 200 200 200 200 200	244444 0000 0000 0000 0000 0000 0000 00
0000 00 00 0	00

## ALIGNMENTS

US-09-954-456-1583

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gequence 1883, Application US/09954456
; Sequence 1883, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANTY YOUNG PAUL
; TITLE OF INVENTION: PROCESS for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT FILING DATE: 2000-09-18
; PRIOR PELICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-20
; PRIOR FILING DATE: 2000-09-20
; PRIOR PELICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR PELICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR PELICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-09-26
; PRIOR FILING DATE: 2000-09-27
; PRIOR PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
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58.1%; Pred. No. 0.01;
iive 0; Mismatches 52;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 58.1
Matches 72; Conservative
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                 417 CAACGTTGCGGACGTGGTAGTGGTGGCGCGTTGGAGCGGTTTGGAGACGGCACGCAA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 AGTCCAGGCCGCCGGTCTGTCCTGCCTCGTTCTTGAGGCGATGGATCGTGTAGGGGGAAA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 AGTCCAGGCCGCCGGTCTGTCCTGCCTCGTTGAGGCGATGGATCGTGTAGGGGGAAA
                                                                                                                                                                                                                                                                     Sequence 2391. Application US/09880107
FPACENT NO. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe.
APPLICANT: Scherf, Uwe.
APPLICANT: Scherf, Uwe.
APPLICANT: Scherf, Uwe.
APPLICANT: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0.
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-106-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEO ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M69177 US-09-880-107-2391
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Patent No. US20020119462A1
CENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Dorter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Gastle, Arthur
APPLICANT: Gastle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038 US
FILE REFERENCE: 44921-5038 US
FILE REFERENCE: 4201-5038 US
FILE REFERENCE: 4201-5038 US
CURRENT FILING DATE: 2001-07-31
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58.1%; Pred. No. 0.01;
tive 0; Mismatches 52;
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Matches 72; Conservative
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US-09-917-800A-1612
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LENGTH: 2491
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1679 AAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAG 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1799 CGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATA 1858
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US-09-917-800A-1612
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Patent No. US20020052308A1

Patent No. US20020052308A1

GENERAL INFORMATION:

TITLE REFERENCE: PA106

CURRENT FILING DATE: 2001-08-10

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

LENGTH: 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0%; Score 39; DB 10; Length 2389; Best Local Similarity 47.7%; Pred. No. 0.039; Matches 114; Conservative 0; Mismatches 125; Indels
                                           PRIOR APPLICATION NUMBER: US 60/22,880
PRIOR FILING DATE: 2001-02
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-05-20
PRIOR FILING DATE: 2001-05-06
PRIOR FILING DATE: 2001-06-13
SPRIOR FILING DATE: 2001-06-13
SOFTWARE: PALENTING NOWER: US 60/293,459
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 1612
LENGTH: 2389
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NAME/KEY: misc_feature
LOCATION: (480)
OTHER INFORMATION: n equals a,t,g, or c
FILING DATE: 2000-07-31
APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Rattus norvegicus
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ORGANISM: Homo sapiens
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0.18;
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Pred. No. 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.9%;
Best Local Similarity 58.9%;
Matches 63; Conservative
                                                                                                                                                          Query Match
Best Local Similarity 56.6%;
Matches 69; Conservative
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US-09-925-302-242/c
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Batt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCACLE AND FAT DEPOSITION
TITLE OF INVENTION TO THE MUSCACLE AND FAT DEPOSITION
TITLE OF INVENTION TO THE MUSCACLE AND FAT DEPOSITION
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                                                                                                                                                                                                                                                                                                                                                                    1184 CAGGTATGCAGTTTGCCATGCCATGTCAAAGGAACTTGTTCCAGGCTCAGTGCACC 1243
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                                                          2.0%; Score 38; DB 10; Length 1386;
llarity 54.6%; Pred. No. 0.058;
Conservative 2; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 200, 329, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
   APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, ID Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-07
; NUMBER OF SEQ ID NOS: 84881
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2399
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61.0%; Pred. No. 0.068;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Bacillus licheniformis
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Matches 61; Conserv
                                                                                            Best Local Similarity Matches 71; Conserv
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US-09-925-301-562
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                                                                                                                                                                                                                                                                                                                                       182 ATGTGGTTATAGTCGGAGCTGGCTGGCCGGACTGACGGCGGCCGAAGTTACTGCAAGACG 241
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APPLICANT: INVAMONATION:

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE,

TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS

FILE REFERENCE: 4703/0F214

CURRENT APPLICATION UNABER: US/09/912,176

CURRENT FILING DATE: 2001/07/24

PRIOR FILING DATE: 1099-01-22

PRIOR FILING DATE: 1199-01-22

PRIOR FILING DATE: 1199-01-22

NUMBER: OF SEQ ID NOS: 2

SOFTWARE: PETCHTON NUMBER: US/09/2261

NUMBER: OF SEQ ID NOS: 2

SEQ ID NO 2
                                                                                                                                                          Gaps
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; Patent No. US20020044941A1
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR PILING DATE: 1999-03-12
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) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB34-060-Q1-E1-E9
US-09-960-352-3971
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                                                                                               Score 37.2; DB 10;
Pred. No. 0.042;
0; Mismatches 53;
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1275 GGCGTCCGGCTGTATAGTACGATCGGCCTCGGGCGCGTGTTCCGAAGCAAAAAGGTGGT 1334
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                                                                                                                                                                                                                                                                                                       Sequence 617, Application US/09925300 Patent No. US20020151681A1
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US-10-044-090-86
; Sequence 86, Application US/10044090
; Patent No. US20020137081A1
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Best Local Similarity 49,5%
Matches 90; Conservative
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US-09-925-300-617
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US-09-925-300-617
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORNE, Darci T.

APPLICANT: Cockley, Joseph G.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2001-66-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-10-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN VEY: 2.1

LENGTH: 1949
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tive 0; Mismatches 68; Indels 0;
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Best Local Similarity 49.5%; Pred. No. 0.79;
Matches 90; Conservative 0; Mismatches 92;
                                                                                                                                  NAME/KEY: misc feature
LOCATION: (125)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (455)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g, or c; NAME/KEY: misc feature; LOCATION: (3276)
COCATION: (3276)
US-09-925-302-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1133 GGTGCGTGCGGTGTCCTCTCAGGT 1156
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NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 52.89
Matches 76; Conservative
                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                LOCATION: (1014)
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US-09-880-107-2388
              SOFTWARE: Paten
SEQ ID NO 242
LENGTH: 3276
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GENERAL INFORMATION:
APPLICANT: OLGA BADdiman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
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                                                           1335 GGTTTCGTTACCGACAACATTGTATCCCACCTTGACATTTTCACCACCTCTTCCCGCCGA 1394
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                                                                                           303 AATGGACCICCICGGAGACCAGTGAACCIGAACCATCACTCACTCACTTGACCAGTC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 AAGTGACAACATCATCATAGAGACGCTGAACCATGAACATTATGAGTGCAAATACGTAAT 422
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823 AAGTGACAACATCATCATAGAGACGCTGAACCATGAACATTATGAGTGCAAATACGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3147;
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GENERAL INCORMATION.

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION. Nucleic Acids, Proteins and Antibodies

TITLE OF INVENTION. Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCI/US00/05988

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 617
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Pred. No. 1.1;
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ORGANISM: Homo sapiens
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1025 CATTTG 1030
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US-10-044-090-339
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                                                                                           Length 4024;
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Sequence 376, Application US/09925301

GENERAL INFORMATION:

APPLICANT: ROSON et al.

TILLE OF INVENTION:

TILLE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 376

LENGTH: 2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 2018;
   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1273213CB1
US-10-044-090-86
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                                                                                         Score 34.8; DB 12;
Pred. No. 1.2;
0; Mismatches 92;
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Pred. No. 1.5;
0; Mismatches
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COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2012)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-376
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1.8%;
Best Local Similarity 48.9%;
Matches 91; Conservative C
                                                                                           Query Match 1.8%;
Best Local Similarity 49.5%;
Matches 90; Conservative
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Sequence 339, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION UNMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 339
LENGTH: 3370
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                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOTHOR, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPERENCE: 44921-5028 WGO
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR PPLICATION NUMBER: US 60/211,379
PRIOR PPLICATION NUMBER: US 60/237,054
PRIOR PLING DATE: 2000-06-14
PRIOR PLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARR: PALENTIN Ver. 2.1
SSQ ID NO 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D82348 US-09-880-107-1744
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Sequence 1744, Application US/09880107 Patent No. US20020142981A1
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ilarity 48.9%;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                            236 AAATTITITITITAGAGACGAIGITCCCCAIGITITCCCAAGCTGGTCTTGAACCCTGGCC 295
                                                                  379 GATGCCACGCCCTGGTGCCAGGACACTCGACCCCAGACATGCGGACGTGGGGTAGTG 438
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1.8%; Score 33.8; DB 10; Length 401;
Best Local Similarity 48.6%; Pred. No. 0.62;
Matches 89; Conservative 1; Mismatches 93; Indels 0
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                         85; Indels
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Patent No. US20020045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/515,716
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1008
Best Local Similarity 50.0%; Pred. No. 2;
Matches 85; Conservative 0; Mismatches
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; ORGANISM: Homo sapiens
US-09-795-668-1008
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	November 12, 2002, 05:30:45; Search time 5080 Seconds (without alignments) 11051.046 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-771-045A-35 1929 1 atggcacttgcaccgagctagcctggtgccagcatag 1929
Scoring table:	OLIGO NUC Gapop 60.0 , Gapext 60.0
Searched:	2054640 segs, 14551402878 residues
Word size :	0
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries 9b\_0a:\*
9b\_htg:\*
9b\_htg:\*
9b\_on:\*
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9b\_ph:\*
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em\_hun:\*
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em\_htgo\_mus:\*
em\_htgo\_other:\* 

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ğ	5447	5474	5449	4/4	5475	5456	483	1424	457	484	466	5455	AK14348Z Sequence AR145462 Sequence	5489	AR145459 Sequence	5486	1408	5461	5488	200	5467	5468	60	5443	5444		AR145440 Sequence AR145453 Sequence	5473	5480	5450	5451 Sequen	15477 Sequenc	15478 Sequen	4 A			linear PAT 08-AUG-2001					ides and related polypeptides	
SUMMARIES	QI 1	AR14546	AR1	ARI	ARL	AR1	AR1	ARI	ARI,	AR1	AR1	AR1	AR1	ARI	AR1	AR1	AR14	ARI	AR14	AR1	AR1	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AR14	AKIA	AK14	APOC	ALIGNMENTS		1929 b	6211434.	7331		T. Yobbell back T. T.	idase polynucleot	A 35 03-APR-2001;
	Length DB		1389	1389	1392	1442	1442	1464	1464	1673	1803	1803	1930	2079	2490	2490	2976	3003	3003	3591	3591	3618	1928	1928	372	372	182	182	7 2 8	28	37	34	34	34	54	137152				5 from	1 GI:15107		ied. 1 to 1929) P., Gilliam.	amine f use	11434-
8 0.19	ore Match	929 10 827 5	324 16.	24 16.	24 IB.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	24 16.	57 8.	57 8.	0.0 0.0 0.0 0.0	24 6.	Э.		; <sub>~</sub> ;	.i.		ı.	۲.	-i -	i -	i -i				Seguence AR145464	:	Unknown. Unknown.	Unclassified 1 (bases 1 Duvick, J.P.	Amino polyol	Patent: U
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QY         961 AAACTTGCCTGCTGTTCTCAGGGGAAACCAGATCACGGGGTCTGCTGGTGGGA 1020		126 126 132 132	OY 1321 AGCARAAGGGGGGGTGTTACCGGAAAATGTATCCGCGCTFGAATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCGATTTCACGATAAACTAATACACATAAAAATCAAAAATCAAAAAAAA	OY 1441 ATAGTCTTCGTATGGGACAACCCGTGGTGGCGCGAACAAGGCTTCTCGGGCGTCCTCCAA 1500	162 162 168 168	A 174 A 174 S 180 S 180	1 CCGTTCAAGTGTG'	OY 1921 GCAGCATAG 1929  Db 1921 GCAGCATAG 1929  RESULT 2  AR145465  LOCUS  AR145465  1929 bp DNA linear PAT 08-AUG-20
FEATURES Location/Qualifiers  Source 11929  Acrganism="unknown"  BASE COUNT 451 a 537 c 532 g 409 t  ORIGIN  Query Match  Query Match  Best Local Similarity 100.0%; Score 1929; DB 6; Length 1929;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ATGGCACTTGCACCGAGCTACATCCACCAAACGTCGCCTCCCCAGCAGGTATTCC 6	Db   61 CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120	241 TACATGGTCGACTACGCCCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 30  241 TACATGGTCGACTACGCCCCGAGCAAACTCACGCAATTGGAGATGGGCTGAAGGTCTACC 30  1 TTGCCTTGACAGCTCCCTTGCACGCTGGTGCCAGTACGGCCTTGGCTTCACC 36	301 TTTGCCCTTGACAGGCTCCTTGCACGCTGGTGCCAGTACCGGCCTTGGCTTCACCT 30 361 GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCCAGACACACAC	AAAGI AAGAC AAGAC TGGAT	601 AATGACAACCAAAGCGAAGTATCCAGATTGTTGAAAGATTCATTTGGAGGGCGAG 66  601 AATGACAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGCGAG 66  601 AATGACAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGCGAG 66  661 CTCCAGAGGACGAAGTATCAATCCATCAAGACACAGAAGACGTACAACCACTACAAGT 72	1 CCTTATGGTGACTCCCCGGTAAGCACATCCACTTGTGTGATGAGACCTCTGTGGAGTGT 21 CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTGTGTGATGAGACCTCTGTGGAGTGT 21 CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTGAGTGTTGTGATAGAACACTCTGTGAGTGTTGTGATGAACACTCTTGTGATGAACACTCTTGTGATGAACTGCTTGTGATGAAGAGAGTTGATGATGAAGAACACTACTTGTGATGAAGAACACTACTTGTGAAAACAACAACAACACTACATCGTCCAAGTGAAGAACACTACATCGTCCAAGTGAACAACAACAACAACAACAACAACAACAACAACAACAAC	841 GGARCTCCTCCCGTATGGTCTCAGCTGAAGAGTATAGCCTTGAAGACCCCAAGGC 9 1

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Duvick,7.P., Gilliam,J.T. and Maddox,J
Amino polyol amine oxidase polynucleot.
and methods of use
Patent: US 6211434-A 37 03-APR-2001;
Location/Qualifiers
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyyo amine oxidase polynucleotides and related polypeptides and methods of use patent: US 6211434-A 10 03-APR-2001;
Location/Qualifiers
             Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Annino polyyol amine oxidase polynucleotides and related polypeptides and methods of use patent: US 6211435-A 5 03-APR-2001;
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Aunio polyol amine oxidase polynucleotides and related polypeptides and methods of use
and methods of use
Patent: US 6211434-A 5 03-APR-2001;
Location/Qualifiers
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1195 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACAGGGTTCGGCGCTC 1254
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Pred. No. 4.6e-168;
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Sequence 5 from patent US 6211434.
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Sequence 5 from patent US 6211435.
AR145474 1 GI:15107341
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370 c 395 g
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Best Local Similarity 99.7%;
Matches 374; Conservative
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Length 1392;

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1 (bases 1 to 1442)
Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
Amino polyol amine oxidase polynucleotides and related polypeptides
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides and and methods of use
Patent: US 6211434-A 7 03-APR-2001;
Location/Qualifiers
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Pred. No. 4.6e-168;
0; Mismatches 1;
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Sequence 7 from patent US 6211435.
AR145475
AR145475.1 GI:15107342
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Sequence 7 from patent US 6211434.
AR145448 1 GI:15107315
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        Query Match
Best Local Similarity 99.7'
Matches 374; Conservative
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Duvick, J.P., Gilliam, J.T., Maddox, J.R., Crasta, O.R. and Folkerts, O. Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use.
Patent: US 6211435-A 10 03-APR-2001;
Location/Qualifiers
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GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
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Pred. No. 4.6e-168;
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Sequence 10 from patent US 62114
ARI45476 GI:15107343
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                                                                                       Score 324; DB 6; 1
Pred. No. 4.6e-168;
0; Mismatches 1;
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and methods of use
Patent: US 6211435-A 7 03-APR-2001;
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US 6211434.
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1. .1464
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1. .1442
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Sequence 20 from patent
AR145456
AR145456.1 GI:15107323
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374; Conservative
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Matches 374; Conservative
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                                                        BASE COUNT
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          JOURNAL
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AR145456
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1 (bases 1 to 1464)
Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. Amino polypol amine oxidase polynucleotides and related polypeptides and methods of undergrand methods of unde
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1270 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
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Pred. No. 4.6e-168;
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Sequence 20 from patent US 6211435.
AR145483
AR145483.1 GI:15107350
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405 c 409 g
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Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use
and methods of use
Patent: US 6211434-A 22 03-APR-2001;
Location/Qualifiers
1. 1803
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Pred. No. 4.5e-168;
0; Mismatches 1;
                                                                    Score 324; DB 6;
Pred. No. 4.5e-168;
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501 c 502 g
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430 c 456 q
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Best Local Similarity 99.7%;
Matches 374; Conservative
                                                                   Query Match 16.8%;
Best Local Similarity 99.7%;
Matches 374; Conservative
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AR145457
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Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.

Amino polypol amine oxidase polynucleotides and related polypeptides and methods of use

Patent: US 6211435-A 16 03-APR-2001;
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                                                                           08-AUG-2001
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                                                                                                                                                                                  Unclassified.

1 (bases 1 to 1673)

Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
Amino polyol amine oxidase polynucleotides
and methods of use
Patent: US 6211434-A 16 03-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                Query Match
16.8%; Score 324; DB 6; I
Best Local Similarity 99.7%; Pred. No. 4.5e-168;
Matches 374; Conservative 0; Mismatches 1;
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Sequence 16 from patent US 6211435.
AR145481
AR145481.1 GI:15107348
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US 6211434.
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430 c 456 q
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AR145454
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ACCESSION VERSION KEYWORDS

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Search completed: November 12, 2002, 07:53:50 Job time : 5088 secs
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                              DEFINITION
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ORIGIN
                                                                               ORGANISM
                                                                                                 REFERENCE
AUTHORS
TITLE
                                      ACCESSION
VERSION
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RESULT 15
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Unclassified.
1 (bases 1 to 1803)

Buvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. Anno polyyol amine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211435-A 22 03-APR-2001;
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                              1609 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
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Pred. No. 4.5e-168;
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Sequence 22 from patent US 6211435
AR145484
AR145484.1 GI:15107351
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Matches 374; Conservative
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(bases 1 to 1930)

Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

Amino polyol anine oxidase polynucleotides and related polypeptides and methods of use
Patent: US 6211434-A 39 03-APR-2001;
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 08-AUG-2001
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Pred. No. 4.5e-168;
0; Mismatches 1;
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from patent US 6211434.
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Matches 374; Conservative
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PCR primer N23259
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21-MAY-1999;
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Compugen Ltd.
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           GenCore version
Copyright (c) 1993 - 2002
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                    The present sequence is that of an isolated nucleic acid, designated ESP002_C2, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58900) capable of degrading fumonish, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycellal DNA using primers based on APAO of E. Spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAX58383-87) and polypeptides (see AAY58900-05) of E. spinifera and AAX58383-87) and polypeptides (see AAY58900-05) of E. spinifera and plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Transgenic plants can be regenerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonish-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonish or of producing the degrading enzymes are provided. Methods for special processing, silage, food crops and the animal feed and rumen migrocaganisms are also disclosed. APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACATCGGCGTAGGCCCAAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACGCTTTGGGCCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180
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                                                                                                                        New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCACTTGCACCGAGCTACATCCACCCCAAACGTCGCCTCCCCAGCAGGGTATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1929 BP; 451 A; 537 C; 532 G; 409 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide is also useful as a selectable marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1929;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                              Claim 1; Page 137-138; 154pp; English
                                                   Maddox JR,
          (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 1929; Conservative
                                                    J.
                                                   Gilliam
                                                                             WPI; 2000-182425/16.
P-PSDB; AAY58900.
                                                    JP,
                                                    Duvick
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CAGGCCGCCGGTCTGTCCTGCCTCGTTCTTGAGGCGATGGATCGTGTAGGGGGAAAGACT
                CTGAGCGTACAATCGGGTCCCGGCAGGACGACTATCAACGACCTCGGCGCTGCGTGGATC
                                                                           AATGACAGCAACCAAAGCGAAGTATCCAGATTGTTTGAAAGATTTCATTTGGAGGGCGAG
                                                                                                                                      CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT
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GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCCAGGACACTCGACCCCCAGACAAC

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Claim 1; Page 139-140; 154pp; English.
                                                                                                                                                                               94.78;
99.98;
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                                                                                                                     New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                       Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                             GTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGAGCAGCAGCAGTATTTCCAAGGA
                                                                                         CCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGGTATATG
                                                                                                                                          GAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA
                                                                                                                                                                                                                                                                        Exophiala spinifera amino polyol amine oxidase ESP002_C3 DNA.
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/note= "contains introns"
/*39..811
/*tag= b
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                                                                                                                                                                                                                            AAZ58383 standard; DNA; 1929
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99US-0135391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duvick JP, Gilliam JT,
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                                                                                                                                                                                Exophiala spinifera
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The present sequence is that of an isolated nucleic acid, designated ESP002_C3, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see ARYS8901) capable of degrading fumonisin, its hydrolysis product API, and related mycotoxins. The DNA was obtained by PCR amplification of ESP002 mycolial DNA using primers based on APAO of E. spinifera ATCC 74269. The invention provides APAO polynucleotides (see AAXS833-87) and polypeptides (see AAYS8900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing plant cells normally susceptible to Fusarium or other toxin-producing cannot a fumonisin-esterase in a transgenic plant, and for producing APAO and a fumonisin-esterase in a transgenic plant, and for systems. Transgenic plants capable of degrading tumonisin or of producing the degrading enzymes are provided. Methods for cops and detoxification of grain, grain processing, silage, food crops and channal feed and rumen microcranisms are also disclosed. APAO.
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Pred. No. 0;
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                                CCTTATGGTGACTCCCCGGTAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT
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1741 GCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800
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                                                                                                                                                                                                                                                                                                                                                                                          transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                              CCGTTCAAGTGTTCATTTCGTTGGAACGAGACGTCTTTAGTTTGGAAAGGGTATATG
                                                                                          GAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide can also be used as a selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                       Amino polyol amine oxidase; fumonisin; mycotoxin; transgen; detoxification; animal feed; silage; selectable marker; ss
                                                                                                                                                                                                                                                                                                                                                          Amino polyol amine oxidase truncated DNA k0n0-395_6.5.
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99US-0135391.
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P-PSDB; AAY58906.
                                                                                                                                                                      1921 GCAGCATAG 1929
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                                                                                                                                                     GCAGCATAG 1929
                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grain or in silage
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21-MAY-1999;
                                                                                                                                                                                                                                                                                                                           23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-2000
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                                                                                                                                                                                                                                                              AAZ58392
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                                                                                                                                                                                                                                RESULT
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Length 1389;

Score 324; DB 21; Pred. No. 1.8e-158;

16.8%; 99.7%;

Best Local Similarity

Query Match

Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;

us-09-771-045a-35.rng

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Gaps

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oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself a antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other funging that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensitaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                               1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; mutant; ss.
                                                                                                                                                                                                                                                                                                                                                 1015 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGGGTCCCAACACGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                             1075 AAGCAGGTACGACAAAAAGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
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                                                                                                                                                                                                                                                                       Length 1389;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                      Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                   Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amine oxidase DNA clone K:trAPAO.
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                                                                                                                                                                                                                                                                     16.8%;
99.7%;
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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.77
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1375 GTGCCAGCAGCATAG 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exophiala spinifera Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200004159-A1
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                                               1015 CAATGGTCCATTACCTGTTTCATGGTCGGAACCCGGGACGGAAGTGGTCCCAACAGTCC 1074
                                                                                          1615 AAGCAGGTACGACAAAAGTCTGTTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                         1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134
                                                                                                                                                       GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                       1135 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1194
                                                                                                                                                                                                                   CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                    AGAACGCCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                                                                                                             Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                              1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                           TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes an Exophiala spinifera aminopolyol amine
      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium -
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding an aminopolyol amine oxidase clone trAPAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..1389
4..4tag a //ttag a //product = "aminopolyol amine oxidase"
   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilliam JT,
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 75-77; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ60630 standard; DNA; 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US15455
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                                                                                                                                                                                                                                                                                                                                                                                                                       1375 GTGCCAGCAGCATAG 1389
                                                                                                                                                                                                                                                                                                                                                                                                        GTGCCAGCAGCATAG 1929
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duvick J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-182426/16.
P-PSDB; AAY68843.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-2000
 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ60630;
 Matches
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                                                                                                                                                                                                                                                1195
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidase primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimiorobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungit that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1018 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGGTCC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1138 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGACGAAGCAGCAGTATTTC 1197
                                                                                                                        Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                     /note= "the amino terminal Lys was added to the protein sequence for optimized expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                        DNA encoding an aminopolyol amine oxidase clone K:trAPAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              /product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilliam JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 82-84; 145pp; English.
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.8%;
99.7%;
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/*tag= a
                           (first entry)
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                                                                                                                                                                                                                     Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-182426/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998;
                         16-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crasta OR,
                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1555
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                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a polynucleotide encoded a truncated, but still functional, amino polyol amine oxidase (K:trAPAO, see AAY5899) of Exophiala spinifera. The polynucleotide was derived from clone k000-395_6.5 (see AAZ5832) to which was added a 5' lysine codon (nucleotides 1-3), since many amine oxidases have a positively charged amino acid near the N-terminus and upstream of a dinucleotide binding capte. The construct allowed heterologous expression of trAPAO in plotha pastoris and maize. The polynucleotides APA58983-87) and polypeptides (see AAY58900-05) of E. spinifera and Rainocladdella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Evaarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transfernic plants, prokaryotic and non-plant eukaryotic systems.

Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.

APAO polynucleotide can also be used as a selectable marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1018 CAATGGTCCATTACCTGTTTCATGGTCGGAGAACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1137
                                                                                                                                                                                                                                              New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.8%; Score 324; DB 21; Length 1392; llarity 99.7%; Pred. No. 1.8e-158; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           Example 7; Page 81-83; 154pp; English.
                                                                                                                        Maddox JR;
                                               (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
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  99US-0135391
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                                                                                                                      Duvick JP, Gilliam JT,
                                                                                                                                                                   WPI; 2000-182425/16.
P-PSDB; AAY58909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 374; Conserv
                                                                                                                                                                                                                                                                                                 grain or in silage
21-MAY-1999;
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Maddox JR;

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Indels

Length 1392;

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RESULT 6 AAZ60633 ID AAZ6

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Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                           1068 CAATGGTCCATTACCTGTTTCATGGTCGGAACCCGGGACGGAAGTGGTCCCAACAGTCC 1127
                                                                                                                                                                                                                        1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
  prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and animal feed and rumen microorganisms are also disclosed. APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1368 TATATGGAAGGGGCCATACGATGGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                          1128 AAGCAGGTACGACAAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                         1188 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGCAGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                    1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1855 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                .;
0
                                                                                                                                           Length 1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding an aminopolyol amine oxidase clone trAPAO-I.
                                                                                                                                                                                Indels
                                                            polynucleotide can also be used as a selectable marker
                                                                                                   Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "aminopolyol amine oxidase"
                                                                                                                                         Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "contains an intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                         Query Match
Best Local Similarity 99.7%;
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number= 1
647..699
/*tag= c
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/*tag= d
/number= 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1428 GTGCCAGCAGCATAG 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200004160-A1
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      8.88888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of polynucleotide k0n0-395_5.4, which encodes a truncated, but still functional, amino polyol amine oxidase (trAPAO-1. see AAY58907 and AAY58908). The polynucleotide was obtained by 3' and 5' RACE PCR using k0n0-395.5 (see AAZ58888), a partial APAO CDNA of Exophiala spinifera. APAO is capable of degrading fumonisin, its hydrolysis product AP1 and related myxotoxins. The invention provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants,
                                                                                                   CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ss.
                      1198 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                              TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                               AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino polyol amine oxidase truncated DNA k0n0-395_5.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "contains an intron"
647..699
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Page 77-79; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                  AAZ58393 standard; cDNA; 1442 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIONEER HI-BRED INT INC CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0092936.
99US-0135391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US15454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182425/16.
P-PSDB; AAY58907, AAY58908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                 1378 GTGCCAGCAGCATAG 1392
                                                                                                                                                                                                                                           GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilliam JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER
(CURA-) CURAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200004159-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duvick JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                    1258
                                                                                                                                                           1855
                                                                                                                                                                                                                                      1915
  1735
                                                                               1795
                                                                                                                                                                                                                                                                                                                                            RESULT 7
AAZ58393
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(first entry)

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New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed
                                                           DNA encoding amino polyol amine oxidase for expression in
                                                                                        Amino polyol amine oxidase; APAO; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; barley; alpha-amylase; signal peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Page 94-96; 154pp; English.

    Exophiala spinifera.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                                                                                                                                              Chimeric - Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182425/16.
P-PSDB; AAY58912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grain or in silage
                                                                                                                                                                                                                                                                                                                                                              WO200004159-A1
                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1999;
                                23-MAY-2000
                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duvick JP,
    AAZ58401;
                                                                                                                                                                             Chimeric
  ö
                                                                                                                                                                                                                                                      The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone,
                                                                                                                                                                                                                                                                                                releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1555 CAATGGTCCATTACCTGTTCATGGTCGGAGGACCGGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1068 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1188 GCCCAAGTCCCAAGGCCGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTC 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          ಭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1128 AAGCAGGTACGACAAAAGTCTGTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1368 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGAGCICCGAGCGCCGICTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1308 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGCAGCACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                         e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                               degrade mycotoxins in plant materials, including expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1442;
                                                                                                                  Maddox JR;
                                                                                                                                                                                      New nucleic acid encoding aminopolyol amine oxidase, used, generaté plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 324; DB 21;
Pred. No. 1.8e-158;
0; Mismatches 1;
                                                                                                                 Gilliam JT,
                                                                                                                                                                                                                                Example 6; Page 78-80; 145pp; English.
                                                                                                                 Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.8%;
99.7%;
                                                                    (PION-) PIONEER HI-BRED INT (CURA-) CURAGEN CORP.
                                         98US-0092936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1915 GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1428 GTGCCAGCAGCATAG 1442
                                                                                                                 Duvick J,
                                                                                                                                          WPI; 2000-182426/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                         P-PSDB; AAY68844
                                        15-JUL-1998;
             08-JUL-1999;
                                                                                                                 Crasta OR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1735
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Maddox JR;

Gilliam JT,

/product= "barley alpha-amylase signal peptide" 73..1461 /\*tag= b

Location/Qualifiers

/\*tag= a

/note= "extra lysine codon"

99WO-US15454 98US-0092936 99US-0135391

/product= "K:trAPAO"
73..75

/\*tag=

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The present sequence is that of a polynucleotide encoding a fusion protein (see AAY58912) composed of the barley alpha-amylase signal peptide and KitzhAPAO (see AAY58909), a truncated, but unctional, amino polyol amino exidase of Exophiala spinifera. The construct was designed for expression and secretion of the construct was designed for expression and secretion of the construct was designed for expression and secretion of its rapable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides (see AAX58383-87) and polypeptides (see AAX58000-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, provexivit and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 16.8%; Score 324; DB 21; Length 1464; Best Local Similarity 99.7%; Pred. No. 1.8e-158; Matches 374; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crops and in animal feed and rumen microorganisms are also on APAO polynucleotide can also be used as a selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
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AAZ58401 standard; cDNA; 1464 BP.

RESULT 9 AAZ58401

2 e.g.

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RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ58395
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                                                                                                                                                                                                                                                                                                                                                δ
δλ
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                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                        Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                1794
                                                                              1854
                                          1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                  1090 CAATGGTCCATTACCTGTTTCATGGTCGGAGGCCGGGACGGAAGTGGTCCCAACAGTCC 1149
                                                                                                    AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                           DNA encoding an aminopolyol amine oxidase for expression in maize.
                                                                       1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGTC
               1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/note= "aminopolyol amine oxidase, with an extra
amino terminal Lys residue for optimized
                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "barley alpha amylase signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maddox JR;
                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilliam JT,
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            expression"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                 AAZ60640 standard; DNA; 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US15455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0092936
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                              73..1461
/*tag= c
                                                                                                                                                              GTGCCAGCATAG 1929
                                                                                                                                                                       Crasta OR, Duvick J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-182426/16.
P-PSDB; AAY68848.
                                                                                                                                                                                                                                                                                                       Synthetic.
Exophiala spinifera.
                                                                                                                                                                                                                                                                                                Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200004160-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-2000
                                                                                                                                                                                                                                              16-MAY-2000
                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                AAZ60640;
                                                                                                     1795
                                                                                                                                                               1915
                                                                                                                                                                                                           AAZ60640
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The present sequence encodes an Exophiala spinifera aminopolyol amine oxidase (APAO). The APAO enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an oxidase family, that oxidise primary amine to an algeby de or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Pusarium or other fungic that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                                                                                                                                                             fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1855 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1090 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1615 AAGCAGGTACGACAAAAGTCTGTGGGACCAACTCCGCGCGGGCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGCCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino polyol amine oxidase (alpha mating factor signal peptide) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGAGCICCGAGCGCCGICIAIGGGCIGAACGAICTCAICACACTGGGIICGGCGCIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 324; DB 21; Length 1464;
Pred. No. 1.8e-158;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS
New nucleic acid encoding aminopolyol amine oxidase, used, generate plants resistant to Fusarium ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino polyol amine oxidase; APAO; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; alpha mating factor; signal peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other;
                                                                                                      Example 11; Page 95-97; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Saccharomyces cerevisiae.
Chimeric - Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ58395 standard; cDNA; 1673 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.8%;
ilarity 99.7%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1915 GTGCCAGCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1450 GTGCCAGCAGCATAG 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ58395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1675
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P-PSDB; AAY68846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998;
                                                                                                                                                                                                                                                                      16-MAY-2000
                                                                                                                                                                                                                                                                                                                      Aminopolyol
                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crasta OR,
                                                                                                                                                                                                                                                AAZ60638;
                                                                                                                                                                                                                                                                                                                                   plant
                   1471
                                           1795
                                                                                         1855
                                                                                                                                                             1651
                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                            AAZ60638
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                                                                                                              ΩD
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of polynucleotide ppiczalphaA:K:trAPAO encoding a protein (see AAY58910) comprising the yeast alpha mating carcor signal peptide (lused with KitaPAO) a truncated, but factor signal peptide (lused with KitaPAO), see also AAY58909) of functional, amino polyol amino exidase (APAO, see also AAY58909) of Exophiala spinifera. The polynucleotide was designed for expression in Pichla pastoris. The encoded protein is capable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see AAZ58900-05) of Expinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, sliage, food crops and in animal feed and rumen microorganisms are also be microorganisms are also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1291 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGAAGTGGTCCCAACAGTCC 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCCAGCCTACGAGAACGCCGGG 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1411 GCCCAAGTCCCCAGAGCCGCCCAACGTGCTCGAAATCGAGTCGAAGCAGCAGCAGTATTC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1735 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó,
                                                                "yeast alpha mating factor secretion signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 324; DB 21; Length 1673; Pred. No. 1.8e-158; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 85-87; 154pp; English.
                                                                                                                                      /*tag= d
/note= "extra lysine"
Location/Qualifiers
1..1665
                                                                                                               "K:trAPAO'
                                                                                                                                                                                                                                                                                                                     Maddox JR;
                                                                                                                                                                                                                                                                                PION-) PIONEER HI-BRED INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used as a selectable marker.
                                                                                                                                                                                                                        99WO-US15454
                                                                                                                                                                                                                                             98US-0092936
                                                                                                                                                                                                                                                          99US-0135391
                                                                                                     /*tag= c
/product= '
268..270
                                                                  /product=
                               a
                                                                                         268..1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.7 Matches 374; Conservative
                              /*tag=
1..267
/*tag=
                                                                                                                                                                                                                                                                                                                   Gilliam JT,
                                                                                                                                                                                                                                                                                            CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                          WPI; 2000-182425/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY58910
                                                                                                                                                                         WO200004159-A1
                                                                                                                           misc_feature
                                                                                                                                                                                                                      08-JUL-1999;
                                                                                                                                                                                                                                                          21-MAY-1999;
                                                                                                                                                                                                                                             15-JUL-1998;
                                                                                                                                                                                                27-JAN-2000
                                           sig_peptide
                                                                                       mat_peptide
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        QQ
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The present sequence encodes a Exophiala spinifera aminopolyol amine oxidase (APAO). The enzyme has homlology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or Ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycocoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi
polyol amine oxidase; APAO; mycotoxin degradation; antimicrobial; fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "aminopolyol amine oxidase"
1..267
/*tag= b
/note= "east alpha mating factor secretion signal"
268..1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding an aminopolyol amine oxidase for expression in Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                    AGAACGCCGTTCAAGTGTGTTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG
                                                                                                                                                                                                         TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding aminopolyol amine oxidase, used, e.g. generate plants resistant to Fusarium -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "aminopolyol amine oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilliam JT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..1665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ60638 standard; DNA; 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US15455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                              1915 GTGCCAGCATAG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duvick J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Exophiala spinifera.
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of

English.

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The present sequence is that of the coding region of full-length amino polyol amine oxidase (APAO) CDNA of Exophiala spinifera 2141.10. APAO is capable of degrading fumonishin, its hydrolysis product API, and related myochoxins. The invention provides APAO polyuncleotides (see AAZ5838-87) and polypeptides (see AAZ58300-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or ther toxin-producing fungus infection. Transgenic plants can be requerated from the transformed plant cells. Also provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for producing APAO enzyme in proxexryctic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Wethods for decoxification of gradin, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide is also useful as a selectable marker.
             New isolated polynucleotides, polypeptides useful for detecting and degrading fumonish or structurally related mycotoxin in processed grain or in silage
                                                                            Example 10; Page 97-100; 154pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ60641 standard; DNA; 1803
                                                                                                                                                                                                                                                                                                                                                                                                 16.8%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 374;
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AAZ60641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1609
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    Q
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that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
                                                                                                                                                                                                                                                                              1351 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCGGGCTACGAGAACGCCGGG 1410
                                                                                                                                                                                                                                                                                                                                        1111 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1470
                                                                                                                                                                                                                                                                                                                                                                                                   1855 TATATGGAAGGGCCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCCTAGCCTG 1914
                                                                                                                                                                                                                                                                                                                         GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1734
                                                                                                                                                                                                                                                                                                                                                                                  CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                              1795 AGAACGCCGTTCAAGTGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
                                                                                                                                                                                                  CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
                                                                                                                                                                                                                                                              1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGACGCCGGG 1674
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                                                                                                                                      ;
0
                                                                                                                                      Length 1673;
                                                                                                                                                                      Indels
                                                                                                          Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exophiala spinifera amino polyol amine oxidase cDNA.
                                                                                                                                      Score 324; DB 21;
Pred. No. 1.8e-158;
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maddox JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ58402 standard; cDNA; 1803
                                                                                                                                    16.8%;
ilarity 99.7%;
Conservative
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P-PSDB; AAY58913.
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                                                                                                                                                     Similarity
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21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2000
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                                                                                                                                                       Best Local Sim
Matches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ58402;
                                                                                                                                        Query Match
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                                                                                                                                  1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCCAACAGTCC 1614
                                                                                                                                                                                                                                                                                                               1675 GCCCAAGTCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGAGCAGTATTTC 1734
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                                                                                                                                                                                                                       1615 AAGCAGGTACGACAAAAGTCTGTGTGTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG
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                                           Length 1803;
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                                                                                       Indels
Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
                                           Score 324; DB 21;
Pred. No. 1.8e-158;
                                                                                       0; Mismatches
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AAZ58384
ID AAZ583
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The APAO enzyme degradese mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, plants own defensive systems. The APAO polymcieotides are used to generate plants (particularly maize) that are resistant to fusarium or char fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensilaging): for recombinant production of APAO polymeptides; as selection markers for plant transformation; and to clayeptides; as selection markers for plant transformation; and to care used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora.
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                                                                                                                                                                                                                  Maddox JR;
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                                               /product= "aminopolyol amine oxidase"
                                                                                                                                                                                                                Gilliam JT,
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           Location/Qualifiers
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/*tag= a
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                                                                                                                           99WO-US15455,
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P-PSDB; AAY68849.
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The present sequence is that of an isolated nucleic acid, designated ESP003_C12, of Exophiala spinifera isolate ESP002, which encodes an amino polyol amine oxidase (APAO, see AAY58902) capable of degrading fumonishi, its hydrolysis product API, and capable of degrading fumonishi, its hydrolysis product API, and capable of degrading fumonishi, its hydrolysis product API, and capable of degrading fumonishi, its based on APAO of E. spinifera arcording primers based on APAO of E. spinifera arcording provides APAO polynucleotides (see AAX5893-87) and polypeptides (see AAX5890-05) of E. spinifera and Phinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing transformed plant cells. The provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for capable of getoxification of grain, grain processing, silage, food crops and in animal feed and rumen microcyanisms are also disclosed. APAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; detoxification; animal feed; silage; selectable marker; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage \,\varepsilon\,
                                                                                                                                                                                                                                                                                                                                                                                                                             Exophiala spinifera amino polyol amine oxidase ESP003_C12 DNA
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/note= "contains introns"
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1134..1187
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Duvick JP, Gilliam JT,
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P-PSDB; AAY58902.
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21-MAY-1999;
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                 Gaps
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Query Match 16.8%; Score 324; DB 21; Length 1930; Best Local Similarity 99.7%; Pred. No. 1.8e-158; Matches 374; Conservative 0; Mismatches 1; Indels 0
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9D\_est2:\*
9D\_htc:\*
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9D\_est4:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em\_gss\_other:\* em\_gss\_pro:\* em\_gss\_rod:\*

em\_gss\_pln: em\_gss\_vrt: em\_gss\_fun: em\_gss\_mam: em\_gss\_mus:

em\_gss\_inv:\*

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Result No. S	O		Query Match Length DB ID	DB	ID	Description
1	23	ŧ	623	17	1.2 623 17 AQ280543	AQ280543 CITBI-E1-
c 0	21	1.1	1284	14	BM803905	BM803905 AGENCOURT
3	20	1.0	285	13	BI050480	BI050480 CM3-GN031
C 4	20	1.0	434	17	AQ046343	AQ046343 RPCI11-34
Ŋ	20	1.0	526	17	3 17 AQ697937	AQ697937 HS_5536_B
9	20	1.0	716	σ	AU133639	AU133639 AU133639

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27		4	AW783945	AL710341	5	BQ805991	9	BE796178	BE714854	BE903091	BF204571	BE714855	BG386968	BG481342	BG386339	BI200064	BE249908	BE267669	BE267625	BF308488	BF306512	BE899487	AW672654	BM835102	BG152936	AA353525	A1414414	BE380159	AA479264	BH317104	AA013604	AI415050	BM829459	AA542887	BI005958	BM755698	AI450161	OVOCAN	-
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## ALIGNMENTS

Department of Eukaryotic Genomics

London Longer (1998)

Longer Meracas: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Longes 1 to 623)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

Unpublished (1998)

Unpublished (1998)

Lother Gess: CITBI-E1-251406.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

Tel: 301 838 0208

Fax: 301 838 0208

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page: 623 bp DNA linear GSS 22-NOV-1998 CITBL-E1-251406.TF CITBL-E1 Homo sapiens genomic clone 251406, DNA sequence. AQ280543 AQ280543 GI:3906362 GSS. Homo sapiens human. RESULT 1 AQ280543 LOCUS DEFINITION ORGANISM JOURNAL ACCESSION REFERENCE AUTHORS VERSION KEYWORDS SOURCE TITLE COMMENT

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sequence tags
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Average insert size 2.1 kb. " 4 others
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CalTech Human BAC Library D"
a 192 c 94 g 200 t 1 others
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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1 (bases 1 to 1284)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov.
Plate: LLAM12184 row: o column: 06
High quality sequence stop: 453.
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Mismatches
                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="251406"
/clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                       Location/Qualifiers
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100.0%; Pre
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Matches 21
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ORIGIN
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BM803905/c
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ORIGIN
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TITLE
JOURNAL
COMMENT
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//organism="Homo saplens"
/db_xref="taxon:9606"
/dbo=_ib=_GN0313"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
/ site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringercy conditions."
73 a 70 c 53 g 89 t
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Butaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 285)
10 Jas Neto.2., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Burustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Bretani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-050101-593-e06&t3=200101-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
BI050480 285 bp mRNA linear EST 15-JUN-2001 CM3-GN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Pred. No.
ive 0; Mismatc
                                                     BI050480
BI050480.1 GI:14458010
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Matches 20; Conservative
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us-09-771-045a-35.rst

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/note="Wector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector and partially digested by the pBACe3.6 vector and the pBACe3.6 vector sites and the pBACe3.6 vector and the pBACe3.6 
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                     library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 112 row: N column: 17
Seg primer: SP6
Class: BAC ends
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Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1112 Col=17 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 17; Length 526;
Pred. No. 35;
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3985
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="OVARC1"
/tissue_type="cvary, tumor tissue"
/tote="Vector: pMEi8SFL3"
/ 197 c 193 g 155 t 3
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/db_xref="taxon:9606"
/clone="OVARC1000332"
                                                                                                                                                                                                                                                                                              High quality sequence stop: 526.
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1..526
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AU133639.1 GI:10994178
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Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. I. (bases I to 434)

Galdan, K. Derry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Goldan, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Unpublished (1998)

L. Ontacri, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdddams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library ovallability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@ressgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
80 9 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 17; Length 434; Pred. No. 33; 0; Mismatches 0; Indels
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University of Washington
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
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/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Scilarity 100.0%; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176 GGTCATTCCAGGTATGCAGT 1195
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hes 20; Conserv
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Gaps

GSS 03-NOV-2001

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2. (bases 1 to 922)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-NUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, VRL:http://hgp.gsc.riken.go.jp/,
Tall:B1-8-503-911, Fax:B1-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                            Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-047F09.R.
Pan troglodytes
                                       AG059979 922 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-047F09.R, genomic survey sequence.
AG059979
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                 Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sec.__intar__inphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
271 c 355 g 243 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 20; DB 17; Length 922; ilarity 100.0%; Pred. No. 39; Conservative 0; Mismatches 0; Indels
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/organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9598"
/clone="PTB-047F09.R"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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Hellantheae; Stevia.

1 (bases 1 to 807)

Is BrandleJ.E., Richman, A., Swanson, A.K. and Chapman, B.P.

Leaf ESTa from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis

L Unpublished (2001)

Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC

Agriculture and Agri-Food Canada - SCPFRC

1391 Sandford St., London, Ontario, CANADA, NSV 4T3

Tel: 519 457 1470

Fax: 519 457 1470

Email: brandleJe@em.agr.ca
Seq primer: 13 promoter primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                BG522272 807 bp mRNA linear EST 01-FEB-2002 2-42 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
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Length 716;
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Score 20; DB 9;
Pred. No. 37;
0; Mismatches
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100.0%; Pre
Query Match 1.0%; So
Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
                                                                                                                1667 ACGCCGGGCCCCAAGTCCCA 1686
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                                                                                                                                                  79 ACGCCGGGGCCCAAGTCCCA 60
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Best Local Similarity 100.C
Matches 20, Conservative
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ORIGIN
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SALK_058617 Arabidopsis thallana TDNA insertion lines Arabidopsis thallana genomic clone SALK_058617, DNA sequence.
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Albaso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 80)
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                                  740 CCCACATCGGCGTAGGCCCA 721
   78
59 CCCACATCGGCGTAGGCCCA
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Gaps

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DKFZp686H1969_r1 686 (synonym: hlcc3) Homo saplens cDNA clone
DKFZp686H1969 5', mRNA sequence.
AL710341
/clone_lib-"Plasmodium yoelii infected liver tissues"
/tissue_type="liver"
/note="Organ: liver; P. yoelii sporozoites were IV
injected into BALB/c mice and livers were harvested 24
hours post injection. Total RNA was processed and
differential display was performed on the infected liver
samples along with uninfected BALB/c liver control."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. Est (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S. Unpublished (1999)
Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DHIOB"
/note="Vector: prriplEx2; Site_1: SfirA; Site_2: SfilB; CDNA-collection"
57 c 64 g 31 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin.
6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemannedArfz-heidelberg.de;
sequenced by EMBL (European Molecular Blology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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This clone (DRRZp688H1965) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                     Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 181;
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/db_xref="taxon:9606"
/clone="DhF2p686H1969"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                     DB 10;
89;
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Pred. No. 98;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
98;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                     1.0%; Score 19;
100.0%; Pred. No.
tive 0; Mismatch
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1..181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0.08; PAR
100.08; PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL710341
AL710341.1 GI:19693696
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                                                                                                                                                                                                                                                                                                           1803 GITCAAGIGIGITCATITC 1821
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                                                                                                                                                                                                                                                                                                                                   43 GTTCAAGTGTGTTCATTTC 61
                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                             Best Local Similarity
Matches 19; Conserv
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LOCUS
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ORIGIN
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BE560457/c
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JOURNAL
COMMENT
                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                   Matches
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AUTHORS
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KEYWORDS
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Euthoria: Rotheria: Sciurognathi; Muridae; Musinae; Mus.

1. (Dases 1 to 119)
S. Lau.A.O.T., Sacci.J.B. Jr and Azad.A.F.
Retrieving parasite specific liver stage gene products in
Plasmodium yoeli! infected livers using differential display
L. Mol. Blochem. Parasitol. 111, 143-151 (2000)

T. 20542037
Contact: Lau, AOT
Dept. of Microbiology and Immunology
University of Maryland, Baltimore Street, BRB 3-034, Baltimore, MD 21201, USA
Tel: 410-706-7066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW783945 119 bp mRNA linear EST 22-NOV-2000 P2T1L6 Plasmodium yoelii infected liver tissues Mus musculus CDNA similar to liver and blood stage P. yoelii antigen, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                    /strain="Columbia" or /strain="Columbia" or /strain="Columbia" or /strain="Columbia" or /clone="Salk_Co86617" or /clone="Salk_Co86617" or /clone="Lib" Arabidopsis thaliana Innes each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 22 c 15 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                           Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atlg47210 and
an annotated exon of Atlg47210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
    Sequence-Indexed Library of Insertion Mutations in the
                     Arabidopsis Genome
Unpublished (2001)
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
Thoulo N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 19; DB 17; Length 80; 100.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACKWARD: CTACAGAGTGGCTTTAATAC
Insert Length: 119 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 82;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"/strain="BALB/c"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: TGTTATAACTGTATTTAC
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100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: alau@umaryland.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW783945
AW783945.1 GI:7838321
EST.
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                                                                                                                                                                                                                                                                               TDNA tagged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 410-706-0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                   Class:
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AW783945
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TITLE
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MEDLINE
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SOURCE
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       TITLE
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g δλ

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1...184
/organism="rriticum aestivum"
/cultivar="Butte 86"
/docne="Whets 86"
/docne="Whets 86"
/docne="Whets 902_003"
/clone=lib="Wheat developing grains cDNa library"
/tissue_type="whole grains"
/dev_stage="3-4 days post anthesis seed"
/dev_stage="4" days post seed and frozen in liquid nitrogen Environment 5 3.7, 8.10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 35, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S.
/developing poly (ADPA RNA S.) (ADPA S.) (A
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
1=15.105595773
Fax: 5105595818
Email: candersnepw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE264866 119-JUL-2000 001194354F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538309 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE264866.1 GI:9138427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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BE264866
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hes 19; Conserv
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Best Local 3
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BE264866/c
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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      COMMENT
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High quality sequence stop: 182.

Location/Qualifiers

1. .182

Location/Qualifiers

1. .182

/dorganism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InhaGE: 368725"
/clone="InhaGE: 368725"
/clone="InhaGE: 368725"
/clone="Lype="Burkitt lymphoma"
/labt_host="Burkitt lymphoma"
/labt_host="Direction 1ymph: yector: poTBJ; Site_1: XhoI; Site_2: Groned into Ecori: yego: yector: poTBJ; Site_1: XhoI; Site_2: Groned into Ecori: yego: sealected >500p for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using zAP-cobA synthesis kit
(Stratagene) and Superscite II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHE3573_E02_J03ZS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3573_E02_J03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticaea; Triticum.

1 (bases 1 to 184)
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, R., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.

The Structure and function of the expressed portion of the wheat genomes - Developing grains cDNA library
Unpublished (2002)
   BE560457 115-AUG-2000 601346723F1 NIH_MGC_8 HOMO sapiens cDNA clone IMAGE:3687725 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM379 row: m column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                     BE560457.1 GI:9804177
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                                                         mRNA sequence.
BE560457
                                                                                                                                                                                                          Homo sapiens
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/db_xref="taxon:9606"
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/clone='Insage:3538309"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: cgapbs-remail.nih.gov
Irissue Procurement: DcrD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM803 row: j column: 05

High quality sequence stop: 201.
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NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Plater LLCM233 row: k column: 14
High quality sequence start: 4
High quality sequence stop: 185.
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100.0%; Pred. No. 98;
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
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Pred. No. 1e+02;
0; Mismatches 0; Indels
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Matches 19; Conservative
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BG52272 AG059979 BH811443 AW783945 AL710341 BE560457 BQ805991 BE264866	BE714854 BE903091 BE903091 BE744855 BG386968 BG481342 BG386386386 BE246908 BE246908 BE246908 BE267659	BE899487 W672654 BM835165936 BG152936 A1414444 BE380159 AA419264 BA479264 AA013604 AA013604 AA15050 BM8428459 AA542887 BIO05558 BIO05558 BIO0558 AA50161 AM504032	ALIGNMENT  623 bp  ITBI-E1 HOMO	2 hordata; C rimates; C S.D., Zhac Suh, E., V	BAC End S 251406.TR oric Genomic Resea
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FEATURES

BASE COUNT

DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 285)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.Y., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                    BIO50480 285 bp mRNA linear EST 15-JUN-2001
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Fax: +55-11-270701
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-
050101-593-e06&t3=3001-01-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
High quality sequence stop: 285.
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/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI;
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI;
/ste_2: SmaI; A mini-ibrary was made by cloning
/products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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RPCI11-34I18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-34I18,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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ORIGIN
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                                                                                                                                                 ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E (1) (abases 1 to 1284)

I (bases 1 to 1284)

L (britishia (1999)

L (britishia (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at;

http://image.llnl.gov

Plate: LLAMISTB4 I www. o column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1284 bp mRNA linear EST 05-MAR-2002 AGENCOURT_6439488 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520605 BM803905
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                                                                                                                                                                                                          /sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
calTech Human BAC Library D"
a 192 c 94 g 200 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="lelomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. 4 others
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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100.0%; Pred. No. 0.81;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Pred. No. 12;
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                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5520605"
/clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                         /db_xref="taxon:9606"
/clone="251406"
/clone_lib="CITBI-E1"
                    Seq primer: Mi3-21
Class: BAC ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTGGTAGTGGTGGCCCTGG 1176
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stches 23; Conservative
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BM803905/c
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Gaps

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BASE COUNT ORIGIN

FEATURES

962

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SERERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-07-25
EARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCGAGCTTGCCTTGCTGCAGTTGGAGCCTCTTCAAACGACGTCACCAAGCTCAATTAC 240
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US-09-352-159-41
US-09-352-159-43
US-09-352-159-15
US-09-352-159-15
US-09-352-168-15
US-09-352-159-45
US-09-352-159-46
US-09-352-168-15
US-09-352-168-15
US-09-352-168-15
US-09-352-168-15
US-09-352-159-13
US-09-352-168-13
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100.0%; Pred. No. 0;
live 0; Mismatches
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US-09-352-159-35
Sequence 35, Application US/09352159A
; Patent No. 6211434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Exophiala spinifera
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NAME/KEY: intron

LOCATION: (1134)...(1186)

US-09-352-159-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcaycomB.seq:*
                    5.1.3
Compugen Ltd.
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US-09-352-159-37
US-09-352-168-5
US-09-352-168-10
US-09-352-168-10
US-09-352-168-7
US-09-352-168-7
US-09-352-168-10
US-09-352-168-20
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US-09-352-168-20
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US-09-352-159-28
US-09-352-168-28
                                                                                                                                                                                                                                                                                                                                                                                                                             441362 seqs, 153338381 residues
                    GenCore version
Copyright (c) 1993 - 2002
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Gapop 60.0 , Gapext 60.0
                                                                                                              nucleic search, using
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vick, Jonathan P.
11iam, Jacob T.
ddx, Joyce R.
NTION: Amino Polyol Amine Oxidase
NTION: Polynucleotides and Related Polypeptides and Methods of Use
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ING DATE: 1999-07-12
LICATION NUMBER: 60/092,936
LICATION NUMBER: 60/135,391
LICATION NUMBER: 60/135,391
ING DATE: 1999-05-21
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LSEQ for Windows Version 3.0
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Patent No. 6211434
GENERAL INFORMATION:
APPLICANT: DUVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
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     Query Match 94.7%;
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Length 1389; Indels

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Sequence 10, Application US/09352159A

Patent No. 6211434
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GIlliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyuclectides and Related Polypeptides and Methods of Use
TITLE REPRENCE: 1134
CURRENT APPLICATION NUMBER: G0/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/135,391
EARLIER FILING DATE: 1999-07-25
SEARLIER APPLICATION NUMBER: 60/135,391
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                           1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
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99.7%; Pred. No. 3.3e-159;
tive 0; Mismatches 1;
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OTHER INFORMATION: Extra lysine in K:traPAO
LENGTH: 1389
TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
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ORGANISM: Exophiala spinifera
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Matches 374; Conservative
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LOCATION: (1)...(1389)
NAME/KEY: misc_feature
LOCATION: (1)...(3)
                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...(1386)
US-09-352-168-5
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US-09-352-159-10
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TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
CURRENT APPLICATION NUMBER: US/09/352,159A
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER PILING DATE: 1998-07-25
EARLIER PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SEATLIER FILING SATE: PASTSEQ for Windows Version 3.0
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US-09-352-168-5
Sequence 5, Application US/09352168A
Sequence 5, Application US/09352168A
September No. 6211435
GENERAL INFORMATION:
APPLICANT: Crasta, Oswald R.
APPLICANT: DOLIVECK, JOHANDARD P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of File Reference: 0875
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Pred. No. 3.3e-159;
0; Mismatches 1;
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EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Exophiala spinifera
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Best Local Similarity 99.7%;
Matches 374; Conservative (
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; LOCATION: (1)...(1386)
US-09-352-159-5
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LENGTH: 1389
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Use

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Sequence 7, Application US/09352159A

Sequence 7, Application US/09352159A

Patent No. 6211434

GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Maddox, Joyce N.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynuclectides and Related Polypeptides and Methods of US
FILE REPERBNCE: 113
CURRENT APPLICATION NUMBER: US/09/352,159A

CURRENT FILING DATE: 1999-07-12

EARLIER FILING DATE: 1998-07-25

EARLIER FILING DATE: 1998-05-21

SAFRIER FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWAME: FastSEQ for Windows Version 3.0
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Pred. No. 3.3e-159;
0; Mismatches 1;
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ORGANISM: Exophiala spinifera
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US-09-352-159-7
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APPLICANT: Crasts. Oswald R.
APPLICANT: DOVICK, Jonathan P.
APPLICANT: POLICETS, Otto
APPLICANT: POLICETS, Otto
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Maino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides of Use
TITLE OF INVENTION NUMBER: US/09/352,168A
CURRENT PILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
BARLIER PILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOSTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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  Pred. No. 3.3e-159;
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LOCATION: (1)...(1389)
NAME/KEY: misc_feature
LOCATION: (1)...(3)
OTHER INFORMATION: Extra lysine in K:trAPAO
US-09-352-168-10
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US-09-352-168-10
Sequence 10, Application US/09352168A
; Patent No. 6211435
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ORGANISM: Exophiala spinifera
Best Local Similarity 99.7%;
Matches 374; Conservative
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Use

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sequence 20, Application US/09352159A

Sequence 20, Application US/09352159A

Patent No. 6211434

GENERAL INFORMATION:
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
APPLICANT: MINION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: Polyoucleotides and Related Polypeptides of Use
TITLE OF INVENTION: NUMBER: 60/092,936

EARLIER PILING DATE: 1999-07-12

EARLIER PILING DATE: 1999-07-22

EARLIER PILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastERD FOR Windows Version 3.0

SERVINE ABSECT FOR Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTIEST INFORMATION: Nucleotide sequence of K:trapho translational OTHER INFORMATION: fusion with barley alpha amylase signal sequence, OTHER INFORMATION: for expression and secretion of the mature trapho OTHER INFORMATION: for maize. Nucleotides 1-72, barley alpha amylase OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine OTHER INFORMATION: residue; nucleotides 76 -1464, trapho cDNA. FRATURE:

NAME/KEY: sig_peptide
LOCATION: (1)...(72)

OTHER INFORMATION: Barley alpha amylase signal sequence
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0; Mismatches
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COTHER INFORMATION: Added lysine residue US-09-352-159-20
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COTHER INFORMATION: K:traPAOCDNA
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1461)
NAME/KEY: misc_feature
                                                                   1428 GTGCCAGCAGCATAG 1442
                                           GTGCCAGCAGCATAG 1929
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Matches 374; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Unknown
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US-09-352-159-20
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APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Duvick, Jonathan P.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of U
FILE REPRENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1999-07-12
EARLIER FILING DATE: 1999-07-25
NUMBER OF SEQ. ID NOS: 33
SOFTWARE: FASESQ for Windows Version 3.0
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1248 CAAGGAGCTCCGAGCGCCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCGGCGCTC 1307
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ORGANISM: Exophiala spinifera
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Matches 374; Conservative
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NAME/KEY: CDS
LOCATION: (700)...(1439)
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NAME/KEY: intron
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APPLICANT: Duvick, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Middox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 1134
                                                                                                                                                              1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGGCGCCTTTAGTTTGGAAAGGG 1389
             1210 GCCCAAGTCCCCAGAGCCGGCCAACGTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTC 1269
                                                                                1390 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1449
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OTHER INFORMATION: yeast alpha mating factor secretion signal.
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CURRENT FILING DATE: 1999-07-12
BARLIER APPLICATION NUMBER: 60/092,936
BERLIER FILING DATE: 1988-07-25
BARLIER APPLICATION NUMBER: 60/135,391
BARLIER FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 16, Application US/09352159A; Patent No. 6211434; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                            1915 GTGCCAGCAGCATAG 1929
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US-09-352-159-16
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LOCATION: (1)
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LENGTH: 1673
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Fatent No. 6211435

GENERAL INFORMATION:
APPLICANT: Crasta, Jouathan P.
APPLICANT: Crasta, Jonathan P.
APPLICANT: Elkerts, Otto
APPLICANT: Elkerts, Otto
APPLICANT: Maddox, Joyce R.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF ENVENTION NUMBER: US/09/352,168A
CURRENT APPLICATION NUMBER: 06/092,936
EMALIER APPLICATION NUMBER: 60/092,936
EMALIER FILING DATE: 1998-07-25
NUMBER OF SEQ ID NOS: 33
SOFTWARE FASTSEQ for Windows Version 3.0
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                          1330 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1389
                                                                                    1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG 1914
                                                                                                          1795 AGAACGCCGTTCAAGTGTGTTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAAGTCCCAGAGCCGGCAACGTGCTCGAAATCGAGTGGTCGAAGCACAGTATTC 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1461)
OTHER INFORMATION: Nucleotide sequence of K:traPAO translational
OTHER INFORMATION: fusion with barley alpha amylase signal sequence,
OTHER INFORMATION: for expression and secretion of the mature traPAO
OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine
OTHER INFORMATION: residue; nucleotides 76 -1464 , traPAO cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGATION: (1)...(72)
OTHER INFORMATION: Barley Alpha Amylase signal seguence.
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Pred. No. 3.3e-159;
0; Mismatches 1;
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CHER INFORMATION: Added lysine residue
US-09-352-168-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (73)...(1464)
OTHER INFORMATION: K:trapaocdna
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                                                                                                                                                                       1915 GTGCCAGCAGCATAG 1929
                                                                                                                                                                                               1450 GTGCCAGCAGCATAG 1464
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Best Local Similarity 99.7;
Matches 374; Conservative
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                                                                                                                                                                                                                                                                             RESULT 10
US-09-352-168-20
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LENGTH: 1464
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1651 GTGCCAGCAGCATAG 1665

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1531 AGAACGCCGTTCAAGAGTGTTCATTTCGTTGGAACGGAGACGTCTTTAGTTTGGAAAGGG 1590

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIVICK, Jonathan P.
APPLICANT: Gilliam, Jacob T.
APPLICANT: Gilliam, Jacob T.
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
TITLE OF INVENTION: POLYOLOGOTIDES: US/09/352,159A
CURRENT APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 06/092,936
EARLIER APPLICATION NUMBER: 06/135,391
EARLIER PILING DATE: 1999-05-21
EARLIER PILING DATE: 1999-05-21
SEQUID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 3.3e-159;
0; Mismatches 1;
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                  RESULT 13
US-09-352-159-22
; Sequence 22, Application US/09352159A
; Patent No. 6211434
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ORGANISM: Exophiala spinifera
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APPLICANT: Crasta, Oswald R.
APPLICANT: Unvick, Jonathan P.
APPLICANT: FOLKERTS, Otto
APPLICANT: Gilliam, Jacob T.
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US-09-352-159-22
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Best Local Similarity
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US-09-352-168-22
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US-09-352-168-16
Sequence 16, Application US/09352168A
Fatent No. 6711435
GENERAL INFORMATION:
APPLICANT: Clasta, Oswald R.
APPLICANT: FOLKETE, Otto
APPLICANT: FOLKETE, Otto
APPLICANT: Gilliam, Jacob T.
APPLICANT: FOLKETE, Otto
APPLICANT: FOLKET
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                           1591 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGTGTGTGCTGCTG 1650
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   1855 TATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTG
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LOCATION: (1)...(267)
OTHER INFORMATION: yeast alpha mating factor secretion signal.
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16.8%; Score 324; DB 4; I
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Exophiala spinifera
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; LOCATION: (1)...(1662)
US-09-352-168-16
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Search completed: November 12, 2002, 07:55:23 Job time : 87 secs
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Best Local Similarity 99.7%;
Matches 374; Conservative (
                Exophiala spinifera
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    TYPE: DNA
ORGANISM: I
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TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Amino Polyol Amine Oxidase
TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
FILE REFERENCE: 0875
CURRENT APPLICATION NUMBER: US/09/352,168A
CURRENT APPLICATION DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER FILING DATE: 1998-07-25
SOFTWARE: FASTEC for Windows Version 3.0
SOFTWARE: FastESC for Windows Version 3.0
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                                                                                                                                                                                                                                                       Length 1803
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Pred. No. 3.3e-159;
0; Mismatches 1;
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Best Local Similarity 99.7%;
Matches 374; Conservative
                                                                                                                                                                           ORGANISM: Exophiala spinifera
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                                                                                                                                                                                                               ; LOCATION: (1)...(1800) US-09-352-168-22
                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                                                                                LENGTH: 1803
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Pred. No. 3.3e-159;
0; Mismatches 1;
HAME/KEY: intron

LOCATION: (739)...(811)

NAME/KEY: intron

LOCATION: (1134)...(1187)

NAME/KEY: misc_feature

LOCATION: (648)...(648)

GOTHER INFORMATION: n = A,T,C or G
US-09-352-159-39
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us-09-771-045a-35.rnpb

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; Sequence 887, Application US/09833263
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US-09-833-263-887
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Sequence 887, App
Sequence 939, App
Sequence 10314, Ap
Sequence 7447, Ap
Sequence 7462, Ap
Sequence 7464, Ap
Sequence 7464, Ap
Sequence 7464, Ap
Sequence 2462, Ap
Sequence 7247, Ap
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Sequence 134, App
Sequence 905, App
Sequence 170, App
Sequence 57, Appl
Sequence 3, Appli
                                                                                         (without alignments)
8346.111 Million cell updates/sec
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                                                                                                                                                   1 atggcacttgcaccgagcta.....gcctggtgccagcagcatag 1929
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                                                                       2002, 05:34:55 ; Search time 82 Seconds
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_DNB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_DNB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-833-263-887

US-09-822-217-939

US-09-833-263-939

US-09-878-574-10314

US-09-878-574-10314

US-09-960-352-7464

US-09-960-352-7464

US-09-964-761-2462

US-09-864-761-247

US-09-864-761-19193

US-09-938-842A-4623

US-09-938-842A-4623

US-09-938-842A-905

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US-09-938-842A-905
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                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                                                                                                                                             OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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                                                                                                                       US-09-771-045A-35
1929
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 24, Appl Sequence 16, Appl Sequence 12039, A Sequence 12039, A Sequence 12759, A Sequence 12759, A Sequence 515, App Sequence 515, App Sequence 2802, App Sequence 666, App Sequence 666, App Sequence 10561, A Sequence 10561, A Sequence 10561, A Sequence 227, App Sequence 22
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APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Yuqiu
APPLICANT: Wing, Gordon E.
APPLICANT: Wing, Gordon E.
APPLICANT: Clapper, John APPLICANT: OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121, 471C13
CURRENT FILING DATE: 2001-08-03
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEC ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.7;
0; Mismatches 0; Indels
                             US-09-779-233-14
US-09-960-352-12039
US-09-960-352-12494
US-09-960-352-12759
US-09-960-352-12759
US-09-960-352-12759
US-09-923-876-515
US-09-923-876-515
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US-09-970-791-845
US-09-770-791-845
US-09-770-791-845
US-09-770-791-845
US-09-770-791-845
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US-09-770-791-845
US-09-770-791-845
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US-09-770-791-866
US-09-770-791-866
US-09-770-791-866
US-09-770-791-88
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US-09-864-761-29869
US-09-960-352-1982
US-09-960-352-9410
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US-09-960-352-9138
US-09-867-701-5519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 887, Application US/09922217
Patent No. US/020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Wangher, Madeleine Joy
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Stolk, John A.
APPLICANT: Sinth, Carole Lynn
APPLICANT: Sinth, Carole Lynn
APPLICANT: King, Gordon E.
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 Best Local Similarity 100.
Matches 19; Conservative
ORGANISM: Homo sapiens
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Clapper, Jonathan D.
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                   GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

CURRENT APPLICATION NUMBER: US/09/933,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE PASSEQ for Windows Version 3.0

SEQ ID NO 887

LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Secrits, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: State, John A.
APPLICANT: Shary, Tongtong
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR INMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR INMUNOTHERAPY AND COMPOUNDS FOR THEIR USE
TILE REFERENCE: 210121.471C13
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
LENGTH: 228
TYPE: DAA
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Mismatches
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US-09-833-263-939
Sequence 939, Application US/09833263; Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 939, Application US/09922217 Patent No. US20020076414A1
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1.0%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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Best Local Similarity 100.4
Matches 19; Conservative
Patent No. US20020110547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-922-217-939
                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapien US-09-833-263-887
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Sequence 10314, Application US/09878574

Sequence 10314, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: La ROSEPH R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Diants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 1999-06-14

PRIOR PPLICATION NUMBER: 09/333,535

PRIOR PPLICATION NUMBER: 09/333,535

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 10314

LENGTH: 239
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Patent No. US20020110548A1

GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Use 12401.94
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR PRILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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APPLICANT: STOIK, JOHN A.

APPLICANT: STOIK, JOHN A.

APPLICANT: Meadler, Wadeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 939

SEQ ID NO 939

LENGTH: 228
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100.0%; Pred. No. 23;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 10;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Glycine max
COTHER INFORMATION: Clone ID: 701103537H1
US-09-878-574-10314
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; SC
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1668 CGCCGGGCCCCAAGTCCCA 1686
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-09-833-263-939
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US-09-878-574-7447
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us-09-771-045a-35.rnpb

Tue Nov 12 09:29:58 2002

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US-09-960-352-4610/c
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US-09-864-761-2462
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
SEQ ID NOS: 15112
SEQ ID NO 7464
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lalgradi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REPERBERGE: D-1 COM
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-06/085,331
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PEL Frogram
SEQ ID NO 1462
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; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158849H1

; NAME/KEY: unsure

; LOCATION: 250, 254, 261, 263

; OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-1462
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Pred. No. 23;
0; Mismatches 0; Indels
                                                                                                                                                 DB 10; Length 261; 23;
                                                                                                                                                                                           Indels
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                                                                                                                                                 Score 17; DB 1
Pred. No. 23;
0; Mismatches
                                                                                  ; OTHER INFORMATION: Clone ID: 701099887H1
US-09-878-574-7447
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Sequence 7464, Application US/09960352
Patent No. US/0020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1462, Application US/09923876 Patent No. US20020013958A1
                                                                                                                                               Query Match 0.9%; Sox
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
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Best Local Similarity 100.0%; P
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                                          TYPE: DNA ORGANISM: Glycine max
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                 US-09-923-876-1462/c
SEQ ID NO 7447
LENGTH: 261
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Sequence 2465, Application US/09864761
Patent No. US2002004876341
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE ERRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Pred. No. 23;
0; Mismatches 0; Indels
                                                                                                                        Length 433;
                                                                                                                                                                      Indels
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; OTHER INFORMATION: Clone ID: 20-LIB3058-021-Q1-K1-E7
US-09-960-352-4610
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3058-049-Q1-K1-H7
US-09-960-352-7464
                                                                                                                     ore 17; DB 10;
red. No. 23;
Mismatches 0
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PRIOR APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-06-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-37
PRIOR FILING DATE: 2001-01-37
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4610, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing
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100.0%; Pre
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Best Local Similarity 100.
                                                                                                                   Query Match 0.99
Best Local Similarity 100.
Matches 17; Conservative
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FALCHI NO. USZUKACAURO USALA ALEL NO. USZUKACAURO USALA APPLICANT: PEND, Sharron G.
APPLICANT: PEND, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: HARZEL, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
US-09-864-761-7247
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2000-01-29
PRIOR PELING DATE: 2000-09-30
PRIOR PELING DATE: 2001-01-29
PRIOR PELING DATE: 2000-09-30
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Pred. No.
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Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Annol
SEQ ID NO 7247
LENGTH: 597
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMBA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMBA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aconica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-06-08-03
PRIOR ELING DATE: 2000-06-03
PRIOR ELING DATE: 2000-06-03
PRIOR ELING DATE: 2000-10-04
PRIOR ELING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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100.0%; Pred. No. 24;
Live 0; Mismatches 0; Indels
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N: EXPRESSED IN HELA, SIGNAL = 70
N: EXPRESSED IN HEART, SIGNAL = 16
NN: EXPRESSED IN HART, SIGNAL = 5.2
NN: EXPRESSED IN LUNG, SIGNAL = 5.5
NN: EXPRESSED IN LUNG, SIGNAL = 5.5
NN: EXPRESSED IN B4474, SIGNAL = 5.5
NN: FYPRESSED IN ADULT LIVER, SIGNAL = 7.5
NN: FYPRESSED IN ADULT FYPRESSED F
                                             PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00662
PRIOR PELICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2001-01-39
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-39
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Patent No. US20020048763A1
      FILING DATE: 2001-01-30
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
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0.9%; Score 17; DB 10; Length 826; 100.0%; Pred. No. 24; 0; Indels tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 24;
                                                            APPLICANT: Matchew, Abraham V.
APPLICANT: Matchew, Abraham V.
APPLICANT: Matchew, Abraham V.
APPLICANT: Machew, Miliam V.
APPLICANT: Heas, William David
APPLICANT: Heas, William David
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neith
APPLICANT: William Davis, Neith
APPLICANT: NOWHER: US/09/770,445
CURRENT APPLICATION NUMBER: US 60/178,472
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ.ID NO 714
LENGTH: 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-714
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ORGANISM: Arabidopsis thaliana
                   Yu, Yang
Rameaka, Joshua G.
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Best Local Similarity 100.(
Matches 17; Conservative
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OTHER INFORMATION: EXPRESSED IN BONE MARCM, SIGNAL = 12

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 9.7

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 70

OTHER INFORMATION: EXPRESSED IN HBLA, SIGNAL = 70

OTHER INFORMATION: EXPRESSED IN HRAN, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2

OTHER INFORMATION: EXPRESSED IN BY41, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN BY44, SIGNAL = 5.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.00+00

OTHER INFORMATION: NT HIT: 9111424380, EVALUE 0.00e+00

US-09-864-761-19133
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR RELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-09-20
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: US 09/774,203
PRIOR PLICATION NUMBER: US 000-09-30
PRIOR PLICATION NUMBER: US 000-0
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Matches 17; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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RESULT 15
US-09-925-301-134/c
| Sequence 134 Application US/09925301
| Patent No. US200200523081
| Patent No. US200200523081
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PANOE
| CURRENT APPLICATION NUMBER: US/09/925,301
| PRIOR APPLICATION NUMBER: COT/US00/05882
| PRIOR PRILOR DATE: 2000-03-08
| PRIOR PRILOR DATE: 2000-03-08
| PRIOR PLICATION NUMBER: 60/124,270
| PRIOR PLICATION NUMBER: 60/124,270
| PRIOR PLICATION NUMBER: 60/124,270
| RIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1694
| SEQ ID NO 134
| LENGTH: 1657
| TYPE: DNA | CORGANISM: Homo sapiens US-09-925-301-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 17; DB 10; Length 1657; Best Local Similarity 100.0%; Pred. No. 25; Matches 17; Conservative 0; Mismatches 0; Indels C
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